

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	2 US-08-147-772-2	Sequence 2, Appli
2	1149	100.0	288	2 US-08-456-104-6	Sequence 6, Appli
3	1149	100.0	288	2 US-08-109-624-23	Sequence 23, Appli
4	1149	100.0	288	2 US-08-751-767A-6	Sequence 6, Appli
5	1149	100.0	288	3 US-08-153-262-2	Sequence 2, Appli
6	1149	100.0	288	3 US-08-479-744A-29	Sequence 29, Appli
7	1149	100.0	288	3 US-08-280-757B-29	Sequence 29, Appli
8	1149	100.0	288	3 US-08-159-135-2	Sequence 2, Appli
9	1149	100.0	288	3 US-08-205-697A-19	Sequence 19, Appli
10	1149	100.0	288	3 US-08-705-525-19	Sequence 19, Appli
11	1149	100.0	288	4 US-08-450-798-2	Sequence 2, Appli
12	1149	100.0	288	4 US-08-403-253A-2	Sequence 2, Appli
13	1149	100.0	288	4 US-09-654-200-13	Sequence 13, Appli
14	1149	100.0	288	4 US-08-667-135-24	Sequence 34, Appli
15	1149	100.0	288	4 PCT-US95-02576-19	Sequence 19, Appli
16	1149	100.0	288	5 PCT-US95-02576-19	Sequence 19, Appli
17	1149	100.0	473	3 US-08-171-945-131	Sequence 131, Appli
18	1102	95.9	208	4 US-03-460-384-36	Sequence 36, Appli
19	1100	95.7	288	4 US-09-654-200-14	Sequence 14, Appli
20	1050	91.4	208	3 US-08-630-172-15	Sequence 15, Appli
21	1050	91.4	208	3 US-09-375-419-15	Sequence 15, Appli
22	743	64.7	292	4 US-09-654-200-16	Sequence 16, Appli
23	743	64.7	292	4 US-08-303-040-2	Sequence 2, Appli
24	739	64.3	292	4 US-09-303-040-4	Sequence 4, Appli
25	738	64.2	299	4 US-09-654-200-15	Sequence 15, Appli
26	561	48.8	306	3 US-08-205-697A-17	Sequence 17, Appli
27	561	48.8	306	3 US-08-205-525-17	Sequence 17, Appli

IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic  
 FEATURE: extracellular domain  
 NAME/KEY: 1 to 208  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: transmembrane domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: intracellular domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: 19 C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: SELL, JEFFREY M.  
 AUTHORS: FREEMAN, GORDON J.  
 AUTHORS: LEE, GRACE  
 AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With  
 JOURNAL: Unique Expression On Activated And Neoplastic B Cells  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
 US-08-147-772-2  
 Query Match 100.0%; Score 1149; DB 2;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 GLSHFCGVIVHTKEKEVATLSCGHNVSVEEELAQTRIYQKEKVKVLTMMSGDMNIVPE 60  
 27 GLSHFCGVIVHTKEKEVATLSCGHNVSVEEELAQTRIYQKEKVKVLTMMSGDMNIVPE 86  
 61 YKQRTIFDITNNISIVIALRPSDEGTYECVVLKYKEKDAFKREHLAEVTLSVKADEFPTPS 120  
 87 YKQRTIFDITNNISIVIALRPSDEGTYECVVLKYKEKDAFKREHLAEVTLSVKADEFPTPS 146  
 121 ISDPEIPTSNIRRICTSGGPPEPHLSWLENELMAINTVSDQPETELYAVSSKLDF 180  
 147 ISDPEIPTSNIRRICTSGGPPEPHLSWLENELMAINTVSDQPETELYAVSSKLDF 206  
 RESULT 2  
 US-08-456-104-6  
 Sequence 6, Application US/08456104  
 Patent No. 5861310  
 GENERAL INFORMATION:  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 APPLICANT: Gray, Gary S.  
 TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE COCKFIELD  
 STREET: 60 State Street, Suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.1, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/456,104  
 FILING DATE:  
 CLASSIFICATION: 424  
 PRIORITY APPLICATION NUMBER: 08/101,624;  
 FILING DATE: 26-JUL-1993;  
 APPLICATION NUMBER: 08/109,393;  
 APPLICATION NUMBER: 19-AUG-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandagouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: RPI-008  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-456-104-6

Query Match 100.0%; Score 1149; DB 2; Length 288;  
Best Local Similarity 100.0%; Pred. No. 7e-113; Indels 0; Gaps 0;  
Matches 216; Conservative 0; Mismatches 0; Feature:

Qy 1 GLSHFCSCVHVTKEYKEVATLSCGHNSVVEELAQTRIYQEKKKVLTMMGDMNIWPE 60  
Db 27 GLSHFCSCVHVTKEYKEVATLSCGHNSVVEELAQTRIYQEKKKVLTMMGDMNIWPE 86

Qy 61 YKNRTIPITNNLSIVIALRSPDEGYECVVLKYEKAFKREHLAEVTLSKADPPTPS 120  
Db 87 YKNRTIPITNNLSIVIALRSPDEGYECVVLKYEKAFKREHLAEVTLSKADPPTPS 146

Qy 121 ISDPEIPTSNIRRICSTSGFFEPHLWLENGEELNAINTVSDPBTELYAVSSKLDF 180  
Db 147 ISDPEIPTSNIRRICSTSGFFEPHLWLENGEELNAINTVSDPBTELYAVSSKLDF 206

Qy 181 NMTTNHSHSPMCLIKYGHLRVNFQENWNTKQEFPPDN 216  
Db 207 NMTTNHSHSPMCLIKYGHLRVNFQENWNTKQEFPPDN 242

RESULT 3  
US-08-101-674-23  
Sequence No. 23, Application US/08101624  
Patent No. 5944607  
GENERAL INFORMATION:  
APPLICANT: Freedman, Gordon J.  
APPLICANT: Nadier, Lee M.  
APPLICANT: Gray, Gary S.  
TITLE OF INVENTION: No. 5944607el CTLA4/CD28 Ligands and  
TITLE OF INVENTION: Uses Therefor  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LATIVE & COCKFIELD  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/101,624  
FILING DATE: 26-JUL-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mandragoras, Amy E.  
REGISTRATION NUMBER: 36 207  
REFERENCE/DOCKET NUMBER: RPI-004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 227-5941  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: B cell activation antigen; natural ligand  
DESCRIPTION: For CD28 T cell surface antigen; transmembrane protein  
FEATURE:  
NAME/KEY: signal sequence

AUTHORS: LEE, GRACE  
 AUTHORS: WHITMAN, JAMES F.  
 AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 23: From -26 to 262  
 US-08-101-624-23

Query Match 100.0%; Score 1149; DB 2; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIVHTKEVKEVATLSCHHNVSVEELAQTQIYQKEBKAVYLTMMSGDMNTYPE 60  
 Db 27 GLSHFCGVIVHTKEVKEVATLSCHHNVSVEELAQTQIYQKEBKAVYLTMMSGDMNTYPE 86

Query Match 100.0%; Score 1149; DB 2; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIVHTKEVKEVATLSCHHNVSVEELAQTQIYQKEBKAVYLTMMSGDMNTYPE 60  
 Db 27 GLSHFCGVIVHTKEVKEVATLSCHHNVSVEELAQTQIYQKEBKAVYLTMMSGDMNTYPE 146

Query Match 100.0%; Score 1149; DB 2; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 YKNRTIFDTNNLSIVIALRPSDEGTYBCVVLKYEKDAFREHLAETVLSYKADEFPPS 120  
 Db 87 YKNRTIFDTNNLSIVIALRPSDEGTYBCVVLKYEKDAFREHLAETVLSYKADEFPPS 146

QY 121 ISDPEIPTSNIRRICSTSQQGPPEBHLSENGEELNAAINTTYSQDPETELYAVSSKDF 180  
 Db 147 ISDPEIPTSNIRRICSTSQQGPPEBHLSENGEELNAAINTTYSQDPETELYAVSSKDF 206

QY 181 NMTTNHSFMCMLIKYGHLYNQTFNWNTTKQEHFPDN 216  
 Db 207 NMTTNHSFMCMLIKYGHLYNQTFNWNTTKQEHFPDN 242

RESULT 5

US-08-153-262-2  
 Sequence 2, Application US/08153262  
 Patent No. 6071716

GENERAL INFORMATION:  
 APPLICANT: FREEMAN, GORDON J.  
 ATTORNEY/AGENT INFORMATION:  
 APPLICANT: FREEMAN, ARNOLD S.  
 APPLICANT: NADLER, LEE M.  
 TITLE OF INVENTION: DNA Encoding B7, A New Member Of The IgG Superfamily With Unique Expression On  
 TITLE OF INVENTION: Of The IgG Superfamily With Unique Expression On  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: The Dana-Farber Cancer Institute  
 STREET: 44 Binney Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02115

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage  
 COMPUTER: IBM Personal System 2; Model 30  
 OPERATING SYSTEM: MS/DOS  
 SOFTWARE: WordPerfect 5.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/153,262  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/751,767-A  
 PATENT NUMBER: US 08751767A  
 FILING DATE: 08-NOV-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SADOFF, B.J.  
 REGISTRATION NUMBER: 36,663  
 TELEPHONE: (203) 259-2846  
 TELEFAX: (203) 255-8900  
 INFORMATION FOR SEQ ID NO: 6:  
 TELEPHONE: 703164091  
 TELEFAX: 703814100  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: for CD28 T cell surface antigen; natural ligand  
 FEATURES:  
 NAME/KEY: signal sequence  
 LOCATION: -34 to -1  
 IDENTIFICATION METHOD: amino terminal sequencing of

US-08-751-767A-6

Query Match 100.0%; Score 1149; DB 2; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIVHTKEVKEVATLSCHHNVSVEELAQTQIYQKEBKAVYLTMMSGDMNTYPE 60  
 Db 27 GLSHFCGVIVHTKEVKEVATLSCHHNVSVEELAQTQIYQKEBKAVYLTMMSGDMNTYPE 86

Query Match 100.0%; Score 1149; DB 2; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 YKNRTIFDTNNLSIVIALRPSDEGTYBCVVLKYEKDAFREHLAETVLSYKADEFPPS 120  
 Db 87 YKNRTIFDTNNLSIVIALRPSDEGTYBCVVLKYEKDAFREHLAETVLSYKADEFPPS 146

Query Match 100.0%; Score 1149; DB 2; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 ISDPEIPTSNIRRICSTSQQGPPEBHLSENGEELNAAINTTYSQDPETELYAVSSKDF 180  
 Db 147 ISDPEIPTSNIRRICSTSQQGPPEBHLSENGEELNAAINTTYSQDPETELYAVSSKDF 206

QY 181 NMTTNHSFMCMLIKYGHLYNQTFNWNTTKQEHFPDN 216  
 Db 207 NMTTNHSFMCMLIKYGHLYNQTFNWNTTKQEHFPDN 242

RESULT 4

US-08-751-767A-6  
 Sequence 6, Application US/08751767A  
 GENERAL INFORMATION:  
 APPLICANT: ANDERSON, ROBERT J.  
 APPLICANT: GRANT, HUGH  
 APPLICANT: MACDONALD, IAN D.  
 TITLE OF INVENTION: INTERLURIN-12 FUSION PROTEIN  
 NUMBER OF SEQUENCES: 80  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHYE P.C.  
 STREET: 1100 NORTH GLEBE ROAD  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22201

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/751,767-A  
 FILING DATE: 08-NOV-1996  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SADOFF, B.J.  
 REGISTRATION NUMBER: 36,663  
 TELEPHONE: (203) 259-2846  
 TELEFAX: (203) 255-8900  
 INFORMATION FOR SEQ ID NO: 6:  
 TELEPHONE: 703164091  
 TELEFAX: 703814100  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: for CD28 T cell surface antigen; natural ligand  
 FEATURES:  
 NAME/KEY: signal sequence  
 LOCATION: -34 to -1  
 IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic  
 FEATURE: extracellular domain

NAME/KEY: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: transmembrane domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE: N-linked glycosylation  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE: N-linked glycosylation  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE: N-linked glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE: Ig V-set domain  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 PUBLICATION INFORMATION:  
 AUTHORS: FREEMAN, GORDON J.  
 AUTHORS: FREEMAN, ARNOLD S.  
 AUTHORS: SEGIL, JEFFREY M.  
 AUTHORS: LEE, GRACE  
 AUTHORS: WHITMAN, JAMES F.

AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
 US-08-153-262-2

Query Match 100.0%; Score 1149; DB 3; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCSCVIVHTKEYKEVATSGHNVSVEEIAATQIYWKERKMWLNMSGDMNTWPE 60  
 Db 27 GLSHFCSCVIVHTKEYKEVATSGHNVSVEEIAATQIYWKERKMWLNMSGDMNTWPE 86

Qy 61 YKNRTIPDITNLNLIVIALRPSDEGTYECVVLKYEKDAFKREHLAETVLSVKADEFPTPS 120  
 Db 87 YKNRTIPDITNLNLIVIALRPSDEGTYECVVLKYEKDAFKREHLAETVLSVKADEFPTPS 146

Qy 121 ISDPEIPTSNIRICSTSGGPPHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 180  
 Db 147 ISDPEIPTSNIRICSTSGGPPHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 206

Qy 181 NMNTNHFSMCLIKYGHLRVNQTFNWNNTTKQEHFPDN 216  
 Db 207 NMNTNHFSMCLIKYGHLRVNQTFNWNNTTKQEHFPDN 242

RESULT 6  
 US-08-479-744A-29  
 Sequence 29, Application US/08479744A  
 Patent No. 6084067  
 GENERAL INFORMATION:  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 APPLICANT: Gray, Gary S.  
 TITLE OF INVENTION: No. 6084067 e1 CTLA4/CD28 Ligands and  
 TITLE OF INVENTION: Uses Therefor  
 NUMBER OF SEQUENCES: 55  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD, LLP  
 STREET: 60 State Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/479,744A  
 FILING DATE: June 7, 1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/280,757  
 FILING DATE: 26-JUL-1994  
 APPLICATION NUMBER: 08/109,393  
 FILING DATE: 28-AUG-1993  
 APPLICATION NUMBER: 08/101,624  
 FILING DATE: 26-JULY-1993  
 APPLICATION NUMBER: 08/147,773  
 FILING DATE: 3-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragoras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: RPI-004CP3  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: B cell activation antigen; natural ligand  
 FEATURE: for CD28 T cell surface antigen; transmembrane protein  
 NAME/KEY: signal sequence  
 LOCATION: -34 to -1  
 IDENTIFICATION METHOD: amino terminal sequencing of  
 OTHER INFORMATION: hydrophobic  
 IDENTIFICATION METHOD: soluble protein  
 NAME/KEY: extracellular domain  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: transmembrane domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: intracellular domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked Glycosylation  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 IDENTIFICATION METHOD: sequence  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig V-set domain

LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 FEATURE:  
 NAME/KEY: Ig C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 PUBLICATION INFORMATION:  
 AUTHORS: FREEMAN, GORDON J.  
 AUTHORS: FREEDMAN, ARNOLD S.  
 AUTHORS: SEGIL, JEFFREY M.  
 AUTHORS: LEE, GRACE  
 AUTHORS: WHITMAN, JAMES F.  
 AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262  
 US-08-479-744A-29

Query Match 100.0%; Score 1149; DB 3; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCSGVIVHTKEVATLSIVLRLPSDEGTYECVVKYEDKDAFREHAAEVTLVMSGDMNIWPE 60  
 Db 27 GLSHFCSGVIVHTKEVATLSIVLRLPSDEGTYECVVKYEDKDAFREHAAEVTLVMSGDMNIWPE 86

Qy 61 YKNRTIFDITNNNSIVLRLPSDEGTYECVVKYEDKDAFREHAAEVTLVMSGDMNIWPE 120  
 Db 87 YKNRTIFDITNNNSIVLRLPSDEGTYECVVKYEDKDAFREHAAEVTLVMSGDMNIWPE 146

Qy 121 ISDPEIPPSNIRRIICSTSGGPPPEHLSWLENGEELNAAINTVSDQPETELYAVSSKLDF 180  
 Db 147 ISDPEIPPSNIRRIICSTSGGPPPEHLSWLENGEELNAAINTVSDQPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCILKYGHLRVNQTFNWNNTIKQEHFPDN 216  
 Db 207 NMTTNHSFMCILKYGHLRVNQTFNWNNTIKQEHFPDN 242

RESULT 7  
 US-08-280-757B-29  
 Sequence 29, Application US/08280757B  
 Patent No. 6130316  
 GENERAL INFORMATION:  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 APPLICANT: Greenfield, Edward  
 APPLICANT: Gary S.  
 TITLE OF INVENTION: No. 6130161 CTLA4/CD28 Ligands and  
 TITLE OF INVENTION: Uses Therefor  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 State Street, Suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/280,757B  
 FILING DATE: 26-JUL-1994

CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/101,624  
 FILING DATE: 26-JULY-1993  
 APPLICATION NUMBER: 08/109,393  
 FILING DATE: 19-AUG-1993  
 APPLICATION NUMBER: 08/147,773  
 FILING DATE: 30-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragoras, Amy E.  
 REGISTRATION NUMBER: 36-207  
 REFERENCE/DOCKET NUMBER: RPI-004CP2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 29:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 MOLECULE TYPE: Protein  
 DESCRIPTION: B cell activation antigen; natural ligand  
 for CD28 T cell surface antigen; transmembrane protein  
 FEATURES:  
 NAME/KEY: signal sequence  
 LOCATION: -34 to -1  
 IDENTIFICATION METHOD: amino terminal sequencing of  
 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
 FEATURES:  
 NAME/KEY: signal sequence  
 LOCATION: -34 to -1  
 IDENTIFICATION METHOD: amino terminal sequencing of  
 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
 FEATURES:  
 NAME/KEY: transmembrane domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic  
 FEATURES:  
 NAME/KEY: extracellular domain  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 FEATURES:  
 NAME/KEY: transmembrane domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic  
 FEATURES:  
 NAME/KEY: intracellular domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 FEATURES:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 FEATURES:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 FEATURES:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: similarity with known  
 FEATURES:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: similarity with known  
 FEATURES:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 FEATURES:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence  
 FEATURE: NAME/KEY: N-linked glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE: NAME/KEY: N-linked glycosylation  
 LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE: NAME/KEY: Ig V-set domain  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE: NAME/KEY: Ig C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 PUBLICATION INFORMATION:  
 AUTHORS: FREEMAN, GORDON J.  
 AUTHORS: FREEDMAN, ARNOLD S.  
 AUTHORS: SEGIL, JEFFREY M.  
 AUTHORS: LEE, GRACE  
 AUTHORS: WHITMAN, JAMES F.  
 AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 29: From -26 to 262  
 US-08-280-757B-29

Query Match 100.0%; Score 1149; DB 3; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCGVIVHVKVEVATLSGHNVSEELAQTIVKREKVLTVMSGDMMNIWPE 60  
 Db 27 GLSHFCGVIVHVKVEVATLSGHNVSEELAQTIVKREKVLTVMSGDMMNIWPE 86

Qy 61 YKNRTIEDITNNLSIVLARSDEGTYECVVLKYEKDAFKREHLLAEVTLVKDFTPS 120  
 Db 87 YKNRTIEDITNNLSIVLARSDEGTYECVVLKYEKDAFKREHLLAEVTLVKDFTPS 146

Qy 121 ISDFEIPTSIRRIICSTSGGPPEPHLSWLENGEELNAINTVSDQDPETELYAVSSKLDF 180  
 Db 147 ISDFEIPTSIRRIICSTSGGPPEPHLSWLENGEELNAINTVSDQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSEFMCLTKYGHLRVQTFNWNNTTKQBFHPDN 216  
 Db 207 NMTTNHSEFMCLTKYGHLRVQTFNWNNTTKQBFHPDN 242

RESULT 8  
 US-09-159-135-2  
 ; Sequence 2, Application US/09159135  
 ; Patent No. 619905  
 GENERAL INFORMATION:  
 APPLICANT: Ostrand-Rosenberg, Suzanne  
 APPLICANT: Baskar, Sivasubramanian  
 APPLICANT: Glimcher, Laurie H.  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadler, Lee M.  
 TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/159,135  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/147,772  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: RPI-003  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7000  
 TELEFAX: (617) 227-5341  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: B cell activation antigen; natural ligand  
 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein

FEATURE:  
 NAME/KEY: signal sequence  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: amino terminal sequencing of  
 IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic

FEATURE:  
 NAME/KEY: extracellular domain  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: intracellular domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: transmembrane domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: Ig V-set domain  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: Ig C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

PUBLICATION INFORMATION:  
 AUTHORS: FREEDMAN, ARNOLD J.  
 AUTHORS: SEGIL, JEFFREY M.  
 AUTHORS: LEE, GRACE  
 AUTHORS: WHITMAN, JAMES F.  
 AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
 US-09-159-135-2

Query Match 100.0%; Score 1149; DB 3;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GISHFCGVIVTHKEKEVATSGVIVSVEILAKTRIYQKEKRVLTMSGDMNWIPE 60  
 Db 27 GISHFCGVIVTHKEKEVATSGVIVSVEILAKTRIYQKEKRVLTMSGDMNWIPE 86

Qy 61 YKNRTIFDITNNLSIVIALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADDFTPS 120  
 Db 87 YKNRTIFDITNNLSIVIALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVKADDFTPS 146

Qy 121 ISDFEIPPSNIRIICSTSGGPPHSLWLENELMAINTVSDPETYAVSSKLDF 180  
 Db 147 ISDFEIPPSNIRIICSTSGGPPHSLWLENELMAINTVSDPETYAVSSKLDF 206

Qy 181 NMTTNHSFMCILKYGHLRVNQTFNWNTTKQEEFPPDN 216  
 Db 207 NMTTNHSFMCILKYGHLRVNQTFNWNTTKQEEFPPDN 242

RESULT 9  
 US-08-105-697A-19  
 Sequence 19, Application US/08205697A  
 Patent No. 6218510  
 GENERAL INFORMATION:

APPLICANT: Sharpe, Arlene H.  
 APPLICANT: Borriello, Francescopaolo  
 APPLICANT: Freeman, Gordon J.  
 APPLICANT: Nadier, Lee M.  
 TITLE OF INVENTION: No. 6218510el Forms of T Cell Costimulatory Molecules and Uses Therefor

NUMBER OF SEQUENCES: 61  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 State Street, Suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 ZIP: 02109-1875

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/205,697  
 FILING DATE: 02-Mar-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: BWI-120CPUS

TELECOMMUNICATION INFORMATION:  
 APPLICATION NUMBER: US/08/205,697A  
 FILING DATE: 02-Mar-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: BWI-120  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)227-7400  
 TELEFAX: (617)227-5941  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein

US-08-205-697A-19

Query Match 100.0%; Score 1149; DB 3; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GLSHFCGSVIVHTKEYKEVATLSGHNSVVELAQTRIYQKEKRNVLTMMSGDNNIWP 60  
 Db 27 GLSHFCGSVIVHTKEYKEVATLSGHNSVVELAQTRIYQKEKRNVLTMMSGDNNIWP 86

Qy 61 YKNRTIFDITNNLSIVLRLRSDEGTYECVVLKYEKDAFKREHLAETVLSYKADEFPTPS 120  
 Db 87 YKNRTIDITNNLSIVLRLRSDEGTYECVVLKYEKDAFKREHLAETVLSYKADEFPTPS 146

Qy 121 ISDFEIPTSNIRRICSTSGGPPEPHLSWLENGEELNAINTVSQDPTETLYAVSSKLDF 180  
 Db 147 ISDFEIPTSNIRRICSTSGGPPEPHLSWLENGEELNAINTVSQDPTETLYAVSSKLDF 206

Qy 61 YKNRTIFDITNNLSIVLRLRSDEGTYECVVLKYEKDAFKREHLAETVLSYKADEFPTPS 120  
 Db 87 YKNRTIDITNNLSIVLRLRSDEGTYECVVLKYEKDAFKREHLAETVLSYKADEFPTPS 146

Qy 121 ISDFEIPTSNIRRICSTSGGPPEPHLSWLENGEELNAINTVSQDPTETLYAVSSKLDF 180  
 Db 147 ISDFEIPTSNIRRICSTSGGPPEPHLSWLENGEELNAINTVSQDPTETLYAVSSKLDF 206

RESULT 11  
 US-09-450-798-2

Sequence 2, Application US/09450798  
 Patent No. 6319709

GENERAL INFORMATION:  
 APPLICANT: Ostrand-Rosenberg, Suzanne  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 State Street, Suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA

APPLICANT: Basikar, Sivasubramanian  
 APPLICANT: Glincher, Laurie H.  
 APPLICANT: Fresman, Gordon J.  
 APPLICANT: Nadier, Lee M.  
 TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity  
 NUMBER OF SEQUENCES: 4

RESULT 10  
 US-08-702-525-19

Sequence 19, Application US/08702525  
 Patent No. 6294660

GENERAL INFORMATION:  
 APPLICANT: Sharpe, Sharpe  
 APPLICANT: Borriello, Francescopaolo  
 APPLICANT: Freeman, Gordon  
 APPLICANT: Nadier, Lee  
 TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory Molecules and Uses Therefor  
 NUMBER OF SEQUENCES: 65  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 28 State Street

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatientIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/4450,798  
 FILING DATE: 29-NOV-1999  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/147,772  
 FILING DATE: 03-NOV-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy B.  
 REGISTRATION NUMBER: 3...;207  
 REFERENCE/DOCKET NUMBER: RPI-003  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: B cell activation antigen; natural ligand  
 for CD28 T cell surface antigen; transmembrane protein  
 FEATURE: signal sequence  
 NAME/KEY: identification METHOD: amino terminal sequencing of  
 LOCATION: -34 to -1  
 IDENTIFICATION METHOD: amino terminal sequencing of  
 DESCRIPTION: B cell activation antigen; natural ligand  
 for CD28 T cell surface antigen; transmembrane protein  
 OTHER INFORMATION: hydrophobic  
 FEATURE: extracellular domain  
 NAME/KEY: identification METHOD: sequence  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: sequence  
 FEATURE: transmembrane domain  
 NAME/KEY: identification METHOD: sequence  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: sequence  
 IDENTIFICATION METHOD: sequence  
 FEATURE: intracellular domain  
 NAME/KEY: identification METHOD: sequence  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: sequence  
 IDENTIFICATION METHOD: sequence  
 FEATURE: N-linked glycosylation  
 NAME/KEY: identification METHOD: sequence  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: sequence  
 IDENTIFICATION METHOD: sequence  
 FEATURE: N-linked glycosylation  
 NAME/KEY: identification METHOD: sequence  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: sequence  
 IDENTIFICATION METHOD: sequence  
 FEATURE: N-linked glycosylation  
 NAME/KEY: identification METHOD: sequence  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: sequence  
 FEATURE: N-linked glycosylation  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: sequence  
 IDENTIFICATION METHOD: sequence  
 FEATURE: N-linked glycosylation  
 NAME/KEY: identification METHOD: sequence  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: sequence  
 IDENTIFICATION METHOD: sequence  
 FEATURE: N-linked glycosylation  
 NAME/KEY: identification METHOD: sequence  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: sequence

IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked Glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig V-set domain  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 PUBLICATION INFORMATION:  
 AUTHORS: FREEMAN, GORDON J.  
 AUTHORS: FREEMAN, ARNOLD S.  
 AUTHORS: SEGIL, JEFFREY M.  
 AUTHORS: LEE, GRAEVE M.  
 AUTHORS: WHITMAN, JAMES F.  
 AUTHORS: NADIER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With  
 Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 US-09-450-738-2  
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
 Query Match 100.0%; Score 1149; DB 4; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113; Indels 0; Gaps 0;  
 Matches 216; Conservative 0; Mismatches 0;  
 Qy 1 GISHFCGVIVHTKEVATLISGHNVSVELAQTIVQKEKAVLUTMSGDMNWIPE 60  
 Db 27 GLSHFCGVIVHTKEVATLISGHNVSVELAQTIVQKEKAVLUTMSGDMNWIPE 86  
 Qy 61 YKNTTIDTNNLISIVIALRPSDEGTYECVVLKYEKDAFKREHLAETVLSYKADFPTPS 120  
 Db 87 YKNTTIDTNNLISIVIALRPSDEGTYECVVLKYEKDAFKREHLAETVLSYKADFPTPS 146  
 Qy 121 ISDFEIPPSNIRRICSTSGGPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 180  
 Db 147 ISDFEIPPSNIRRICSTSGGPPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 206  
 Qy 181 NMNTNHSPMCLIKYGLRVNQTFNNTKQHEFPDN 216  
 Db 207 NMNTNHSPMCLIKYGLRVNQTFNNTKQHEFPDN 242  
 RESULT 12  
 US-08-03-253A-2  
 Sequence 2, Application US/08403253A  
 Patent No. 635694  
 GENERAL INFORMATION:  
 APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.  
 APPLICANT: Gray, Gary S., Rennert, Paul D.  
 TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAIVE & COCKFIELD  
 STREET: 28 State Street  
 CITY: Boston  
 STATE: Massachusetts

COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/403,252A  
 FILING DATE: March 10, 1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/253,964  
 APPLICATION NUMBER: US 08/073,223  
 FILING DATE: 4 JUNE 1993  
 APPLICATION NUMBER: US 08/200,947  
 FILING DATE: 2 FEB 1994  
 APPLICATION NUMBER: US 07/864,805  
 FILING DATE: 7 APR 1992  
 APPLICATION NUMBER: US 08/247,505  
 FILING DATE: 23 MAY 1994  
 APPLICATION NUMBER: US 07/864,807  
 FILING DATE: 7 APR 1992  
 APPLICATION NUMBER: US 07/902,467  
 FILING DATE: 1 JUNE 1992  
 APPLICATION NUMBER: US 07/275,433  
 FILING DATE: 23 NOV 1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragoras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: RPI-002CP2  
 TELECOMMUNICATION: INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 742-4214  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TOPOLogy: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: B cell activation antigen; natural ligand and transmembrane protein  
 FEATURE:  
 NAME/KEY: signal sequence  
 LOCATION: -34 to -1  
 IDENTIFICATION METHOD: amino terminal sequencing of  
 OTHER INFORMATION: soluble protein  
 FEATURE:  
 NAME/KEY: extracellular domain  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 FEATURE:  
 NAME/KEY: transmembrane domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: intracellular domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence

FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 55 to 57  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 192 to 194  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig V-set domain  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig V-set domain  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 PUBLICATION INFORMATION:  
 AUTHORS: FREEMAN, GORDON J.  
 AUTHORS: FREEDMAN, ARNOLD S.  
 AUTHORS: SEGIL, JEFFREY M.  
 AUTHORS: LEE, GRACE  
 AUTHORS: WHITMAN, JAMES F.  
 AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With  
 TITLE: Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
 US-08-403-253A-2

Query Match 100.0%; Score 1149; DB 4; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GLSHFCSGVIIHTVKKEYVATLPSGCHNSVVEELAQTRIYQKEKRNVLTMMSGDNNIWPE 60  
 27 GLSHFCSGVIIHTVKKEYVATLPSGCHNSVVEELAQTRIYQKEKRNVLTMMSGDNNIWPE 86

Qy 61 YKNRTIFDITNNLSIVIALRPSDGEYECVVLKYEKDAFKREHLAEVTLSVKADDEPTPS 120  
 Db 87 YKNRTIFDITNNLSIVIALRPSDGEYECVVLKYEKDAFKREHLAEVTLSVKADDEPTPS 146

Qy 121 ISDFFIPSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 180  
 Db 147 ISDFFIPSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCILKYGHLRVNQTFNWNNTKQEHFPDN 216  
 Db 207 NMTTNHSFMCILKYGHLRVNQTFNWNNTKQEHFPDN 242

RESULT 13  
 US-09-651-200-13  
 ; Sequence 13, Application US/09651200  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Green et al  
 ; TITLE OF INVENTION: Polynucleotides Encoding Members of the Human B  
 ; TITLE OF INVENTION: Lymphocyte Activation Antigen B-7 Family and  
 ; TITLE OF INVENTION: Polypeptides Encoded Theraby  
 ; FILE REFERENCE: 11966-562 (CURA-62)  
 ; CURRENT APPLICATION NUMBER: US/09/651-200  
 ; CURRENT FILING DATE: 2000-08-30  
 ; PRIOR APPLICATION NUMBER: 60/152583  
 ; PRIOR FILING DATE: 1999-09-03  
 ; PRIOR APPLICATION NUMBER: 60/172909  
 ; PRIOR FILING DATE: 1999-12-21  
 ; PRIOR APPLICATION NUMBER: 60/183578  
 ; PRIOR FILING DATE: 2000-02-18  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 13  
 ; LENGTH: 288  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; SEQ ID NO: 13-20-13

Query Match 100.0%; Score 1149; DB 4; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCGVTHVKVEVATLSGCHNYSVEELAQTRLYWQEKVKMVLTMMSGDMNITWPE 60  
 Db 27 GLSHFCGVTHVKVEVATLSGCHNYSVEELAQTRLYWQEKVKMVLTMMSGDMNITWPE 86

Qy 61 YKNRTIFDITNNLSIVILALRPSDEGTYBCVVKYERKDAFKREHLAETVLSKADFPPTPS 120  
 Db 87 YKNRTIFDITNNLSIVILALRPSDEGTYBCVVKYERKDAFKREHLAETVLSKADFPPTPS 146

Qy 121 ISDFFIPSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 180  
 Db 147 ISDFFIPSNIRRICSTSGGFPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLDF 206

Qy 181 NMTTNHSFMCILKYGHLRVNQTFNWNNTKQEHFPDN 216  
 Db 207 NMTTNHSFMCILKYGHLRVNQTFNWNNTKQEHFPDN 242

RESULT 15  
 US-09-435-816A-2  
 ; Sequence 2, Application US/08435816A  
 ; Patent NC: 6534055  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Juns, Carl H.  
 ; APPLICANT: Thompson, Craig B.  
 ; APPLICANT: Nabel, Gary J.  
 ; APPLICANT: Gray, Gary S.  
 ; APPLICANT: Remert, Paul D.  
 ; TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: LAHIE & COCKFIELD  
 ; STREET: 60 State Street, Suite 510  
 ; CITY: Boston  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/435,816A  
 ; FILING DATE: May 4, 1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/403,253  
 ; FILING DATE: 10 MARCH 1995  
 ; APPLICATION NUMBER: US/08/253,964  
 ; FILING DATE: 3 JUNE 1994  
 ; APPLICATION NUMBER: US/08/073,223  
 ; COMPUTER: IBM PC compatible  
 ; FILING DATE: 4 JUNE 1993  
 ; APPLICATION NUMBER: US/08/200,947  
 ; FILING DATE: 23 FEB 1994  
 ; APPLICATION NUMBER: US/07/854,805  
 ; FILING DATE: 7 APR 1992  
 ; APPLICATION NUMBER: US/08/247,505  
 ; FILING DATE: 23 MAY 1994  
 ; APPLICATION NUMBER: US/07/864,866  
 ; FILING DATE: 7 APR 1992  
 ; APPLICATION NUMBER: US/08/218,155  
 ; FILING DATE: 25 MAR 1994  
 ; APPLICATION NUMBER: US/07/864,807  
 ; FILING DATE: 7 APR 1992

RESULT 14  
 US-09-667-135-34  
 ; Sequence 34, Application US/09667135  
 ; Patent No. 6521749  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kyriaki Dunusi-Joannopoulos  
 ; TITLE OF INVENTION: Novel G150 Molecules And Uses Therefor  
 ; FILE REFERENCE: GIN-107  
 ; CURRENT APPLICATION NUMBER: US/09/667,135  
 ; CURRENT FILING DATE: 2000-09-21  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 34  
 ; LENGTH: 288  
 ; TYPE: PRT.

APPLICATION NUMBER: US 07/902,467  
 FILING DATE: 16 JUNE 1992  
 APPLICATION NUMBER: US 07/275,433  
 FILING DATE: 23 NOV 1988  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REFERENCE NUMBER: 36, 207  
 REFERENCE/DOCKET NUMBER: RPI-002CP3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-7400  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 DESCRIPTION: B cell activation antigen; natural ligand;  
 DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein  
 FEATURE:  
 NAME/KEY: signal sequence  
 LOCATION: -34 to -1  
 IDENTIFICATION METHOD: amino terminal sequencing of  
 IDENTIFICATION METHOD: soluble protein  
 OTHER INFORMATION: hydrophobic  
 FEATURE:  
 NAME/KEY: extracellular domain  
 LOCATION: 1 to 208  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: transmembrane domain  
 LOCATION: 209 to 235  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: intracellular domain  
 LOCATION: 236 to 254  
 IDENTIFICATION METHOD: similarity with known  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 19 to 21  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 64 to 66  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 152 to 154  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 173 to 175  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 177 to 179  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 192 to 194

IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: N-linked glycosylation  
 LOCATION: 198 to 200  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig V-set domain  
 LOCATION: 1 to 104  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 FEATURE:  
 NAME/KEY: Ig C-set domain  
 LOCATION: 105 to 202  
 IDENTIFICATION METHOD: similarity with known  
 IDENTIFICATION METHOD: sequence  
 PUBLICATION INFORMATION:  
 AUTHORS: FREEMAN, GORDON J.  
 AUTHORS: FREEDMAN, ARNOLD S.  
 AUTHORS: SEGIL, JEFFREY M.  
 AUTHORS: LEE, GRACE  
 AUTHORS: WHITMAN, JAMES F.  
 AUTHORS: NADLER, LEE M.  
 TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells  
 JOURNAL: The Journal of Immunology  
 VOLUME: 143  
 ISSUE: 8  
 PAGES: 2714-2722  
 DATE: 15-OCT-1989  
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262  
 US-08-435-816A-2  
 Query Match Score 1149; DB 4; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 7e-113;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GLSHFCSGVIVHTKEYKEVATLPSDEGTSGCHNVSBEAQPRIYQKEKRNVLTMNSGDMINIWPE 60  
 Db 27 GLSHFCSGVIVHTKEYKEVATLPSDEGTSGCHNVSBEAQPRIYQKEKRNVLTMNSGDMINIWPE 86  
 Qy 61 YKNRTIFDITNNLSIVLAIRPSDEGTGCVLKYKEVDAFKREHAAEVTLVSKADFPTPS 120  
 Db 87 YKNRTIFDITNNLSIVLAIRPSDEGTGCVLKYKEVDAFKREHAAEVTLVSKADFPTPS 146  
 Qy 121 ISDFEIPTSNIRRICKSTSGGFPEPHLSWLNGEELNAINNTSQDPETELYAVSKLDF 180  
 Db 147 ISDFEIPTSNIRRICKSTSGGFPEPHLSWLNGEELNAINNTSQDPETELYAVSKLDF 206  
 Qy 181 NMNTNISFMCILKYGHLRVNOTPNWNTTKQBFHPDN 216  
 Db 207 NMNTNISFMCILKYGHLRVNOTPNWNTTKQBFHPDN 242  
 RESULT 16  
 PCT-US95-02576-19  
 Sequence 19, Application PC/TUS9502576  
 GENERAL INFORMATION:  
 APPLICANT:  
 TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules  
 NUMBER OF SEQUENCES: 65  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LAHIVE & COCKFIELD  
 STREET: 60 State Street, suite 510  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02109-1875  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION NUMBER: PCT/US95/02576  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/205,697  
 FILING DATE: 02-Mar-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mandragouras, Amy E.  
 REGISTRATION NUMBER: 36,207  
 REFERENCE/DOCKET NUMBER: BWI-120COPPC  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 227-5940  
 TELEFAX: (617) 227-5941  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 PCT-US95-02576-19

Query Match 100.0%; Score 1149; DB 5; Length 288;

Best Local Similarity 100.0%; Pred. No. 7e-113; Mismatches 0; Indels 0; Gaps 0;

Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 GLSHFCGIVHVTKEVKEVATLSCHNVSEELAQTRIYKEKAFKREHLAETVLSYKADFPPS 60  
 Db 27 GLSHFCGIVHVTKEVKEVATLSCHNVSEELAQTRIYKEKAFKREHLAETVLSYKADFPPS 86Query 61 YKNRTIFDITNNLSIVIALRPSDEGTYCVVLYKEKAFKREHLAETVLSYKADFPPS 120  
 Db 87 YKNRTIFDITNNLSIVIALRPSDGTYCVVLYKEKAFKREHLAETVLSYKADFPPS 146Query 121 ISDFEIPTSNIRRICSTSGFPPEHLSWLENGELNAINTVSDPTELYAVSSKDF 180  
 Db 147 ISDFEIPTSNIRRICSTSGFPPEHLSWLENGELNAINTVSDPTELYAVSSKDF 206Query 181 NMTTNHSFMCILKYGLRVNQTFNWNTTKQEHFPDN 216  
 Db 207 NMTTNHSFMCILKYGLRVNQTFNWNTTKQEHFPDN 242

RESULT 17  
 US-09-171-945-131  
 Sequence 131, Application US/09171945  
 Patent No. 6277599

GENERAL INFORMATION:

APPLICANT: Emery, Stephen

APPLICANT: Copley, Clive

APPLICANT: Michael Derek

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said  
 TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System  
 FILE REFERENCE: Monoclonal Antibody to CEA  
 CURRENT APPLICATION NUMBER: US/09/171,945

PRIOR APPLICATION NUMBER: GB8703103.3

PRIOR FILING DATE: 1997-02-14

PRIOR APPLICATION NUMBER: GB8609405.7

PRIOR FILING DATE: 1996-05-04

PRIOR APPLICATION NUMBER: PCT/GB97/01165

PRIOR FILING DATE: 1997-04-29

NUMBER OF SEQ ID NO: 131

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO: 131

LENGTH: 473

TYPE: PCT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: humanized  
 US-09-171-945-131



FT	Misc-difference	186..188	XX	AAW38414;
FT	Misc-difference	207..209	AC	
FT	Misc-difference	/label= see above	XX	
FT	Misc-difference	211..213	DT	08-APR-1998 (first entry)
FT	Misc-difference	/label= see above	XX	
FT	Misc-difference	226..228	DB	B7-1.
FT	Misc-difference	/label= see above	XX	
FT	Misc-difference	232..234	KW	Screening; inhibitor; enhancer; binding; CD28; B7-1.
FT	Misc-difference	/label= see above	XX	
FT	Domain	35..138	OS	Homo sapiens.
FT	Domain	/label= Ig V-set domain	XX	
FT	Domain	139..236	PN	EP79554-A2.
FT	Domain	/label= Ig C-set domain	XX	
XX	WO9503408-A1.	XX	PD	17-SEP-1997.
XX	02-FEB-1995.	XX	PF	04-MAR-1997; 97EP-0301438.
XX	02-FEB-1995.	XX	PR	02-OCT-1996; 96JP-0262085.
XX	26-JUL-1994;	XX	PR	05-MAR-1996; 96JP-0047795.
XX	26-JUL-1994;	XX	PA	(TAKE ) TAKEDA CHEM IND LTD.
XX	19-AUG-1993;	XX	PA	
PR	19-AUG-1993;	XX	PI	Hattori M, Hida T, Kurokawa T, Nakaniishi A;
PR	03-NOV-1993;	XX	XX	
PR	03-NOV-1993;	XX	DR	WPI; 1997-450803/42.
XX	03-NOV-1993;	XX	DR	N-PSDB; AAT96358.
XX	(DAND ) DANA FARBER CANCER INST INC.	XX	PT	New xanthene derivatives useful as immunomodulators - e.g. methyl
XX	(REPK ) REPLIGEN CORP.	XX	PT	2-(carboxymethylsulphonyl)-5,7-dichloro-3,8-dihydroxy-6-
XX	Freeman GJ, Gray GS, Greenfield E, Nadler LM;	XX	PT	carboxylic acid-1-carboxylate.
XX	WPI; 1995-07236/10.	XX	XX	DR; 9-oxo-9-H-xanthene-1-carboxylate.
DR	N-PSDB; AAO81371.	XX	PS	Disclosure; Fig 4; 117pp; English.
XX	PT	XX	XX	The present sequence was used in the development of a novel method
PT	PT	XX	CC	for screening for compounds that inhibit or enhance binding of CD28
XX	PT	XX	CC	to B7-1.
XX	PS	XX	XX	Sequence 288 AA;
XX	PS	XX	Query Match 100.0%; Score 1149; DB 18;	
CC	Q81371 is in pCDM8 vector. It is derived from lymphoid B cells,	XX	Best Local Similarity 100.0%; Pred. No. 3.4e-103; Length 288;	
CC	cell line Raji, clone no. 13. Its position in the genome is	CC	Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CC	chromosome/segment 3. It was published by Freeman, F.J. et al.,	CC		
CC	J. of Immunology 143: 8; 2714-2722, 15th October 1999. It can be	CC		
CC	found in Genbank at Accession no. M27533.	CC	QY 1 GLSHFCGSYIHTVKEVKEYATLSCHNVSVEELAQTRIYQKEKRMVLTMSGDNINWPE	60
CC	The encoded protein, R67989, binds both human CTLA4 and human CD28. It is related	CC	DB 27 GLSHFCGSYIHTVKEVKEYATLSCHNVSVEELAQTRIYQKEKRMVLTMSGDNINWPE	86
CC	to human hB7-2 (see Q81351) and murine hB7 (see Q81372).	CC		
XX	(Updated on 25-MAR-2003 to correct PN field.)	XX	QY 61 YKNRTIIFDTNNLSIVILALRPSDEGTYECVVLKYKEKRMVLTMSGDNINWPE	120
XX	Sequence 288 AA;	XX	DB 87 YKNRTIIFDTNNLSIVILALRPSDEGTYECVVLKYKEKRMVLTMSGDNINWPE	146
CC	Query Match 100.0%; Score 1149; DB 16;	CC		
CC	Best Local Similarity 100.0%; Pred. No. 3.4e-103;	CC		
CC	Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC		
CC	1 GLSHFCGSYIHTVKEVKEYATLSCHNVSVEELAQTRIYQKEKRMVLTMSGDNINWPE	CC		
CC	27 GLSHFCGSYIHTVKEVKEYATLSCHNVSVEELAQTRIYQKEKRMVLTMSGDNINWPE	CC		
CC	61 YKNRTIIFDTNNLSIVILALRPSDEGTYECVVLKYKEKRMVLTMSGDNINWPE	CC	QY 1.81 NMTTNHSFMCLIKYGHLRVQNTWNNTKQEHFPDN 216	
CC	87 YKNRTIIFDTNNLSIVILALRPSDEGTYECVVLKYKEKRMVLTMSGDNINWPE	CC	DB 207 NMTTNHSFMCLIKYGHLRVQNTWNNTKQEHFPDN 242	
XX	RESULT 3	XX		
XX	AAW67804	XX		
XX	ID AAW67804 standard; Protein; 288 AA.	XX		
XX	AC AAW67804	XX		
XX	DT 13-APR-1999 (first entry)	XX		
XX	DE Human B7 protein sequence.	XX		
XX	KW Human; B7; transfection; mammal; tumour cell; sarcoma; co-stimulation;	XX		
XX	T- cell; CD28; CTLA4; ligand; T-lymphocyte response; metastasis.	XX		



Db 87 YKNRTIDITNNLSIVTLALRPSDEGTYCIVLKYERDAFREHLAEVTLSVRADEFTPPS 146  
 CC (macrophage). The fusion proteins or peptides are useful for enhancing or  
 CC suppressing T cell-mediated immune responses, e.g. in situations of  
 CC tissue, skin or organ transplantation, or in graft-versus-host disease.  
 CC The Proteins are also useful for enhancing the efficacy of vaccination  
 CC against a variety of pathogens, and may also be used to upregulate an  
 CC immune response against a particular pathogen during an infection or  
 CC against a tumour in a tumour-bearing host.  
 XX

Db 207 NMTTNHSFMCILKYGHLRVNTQFNNTTKQEHFPDN 242  
 SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 21; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 3 4e-103;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCSGVTHVTKREVATLSGHNNYSVVEELAQTRLYQKEKVMVLTMMGDMNTPWE 60  
 AC 27 GLSHFCSGVTHVTKREVATLSGHNNYSVVEELAQTRLYQKEKVMVLTMMGDMNTPWE 86

Db 28-MAR-2001 (first entry)  
 XX  
 DE Human B lymphocyte antigen B7-1.  
 KW Immunomodulator; fusion protein; human; murine; mouse; lymphocyte; CD28;  
 KW antigen; extracellular domain; CT44; immunoglobulin constant region;  
 KW immunogenicity; tumour; sarcoma; antigen presenting cell; macrophage;  
 KW T cell-mediated immune response; transplantation; vaccination.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6130316-A.  
 PD 10-OCT-2000.  
 XX  
 PF 26-JUL-1994; 94US-0280757.  
 XX  
 PR 26-JUL-1993; 93US-0101624.  
 PR 19-AUG-1993; 93US-010393.  
 PR 03-NOV-1993; 93US-0147773.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 PA (REPK ) REPLICEN CORP.  
 XX  
 PI Freeman GJ, Nadler LM, Gray GS, Greenfield E;  
 XX  
 WPI: 2000-655681/63.  
 DR N-PSDB; AAC84051.  
 XX  
 PR Nucleic acids and fusion proteins of CTLA4/CD28 ligands, useful for  
 PR enhancing or suppressing T cell-mediated immune responses, especially  
 PR during tissue, skin or organ transplantation, or in graft-versus-host  
 PR disease -  
 XX  
 PS Disclosure: Column 87-90; 83pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid molecule encoding a first  
 CC fusion protein comprising a first nucleotide sequence encoding a first  
 CC peptide, and a second nucleotide sequence encoding a second peptide;  
 CC the first nucleotide sequence hybridizes in 6 X sodium chloride/sodium  
 CC citrate (SSC) at 45 deg. C, followed by a wash in 0.2 X SSC at 50 deg. C  
 CC to a portion of a nucleotide sequence which encodes a human or murine  
 CC B lymphocyte antigen (B7-2) extracellular domain. The first peptide has  
 CC the ability to bind CD28 or CTLA4. The first peptide has an amino acid  
 CC sequence that is identical or at least 50% identical with the  
 CC extracellular domain of a human B7-2 peptide (AB37085). The second  
 CC peptide is especially an immunoglobulin constant region. This sequence  
 CC represents the human B lymphocyte antigen B7-1. The sequence is used for  
 CC comparison with the B7-2 sequence. The human B7-2 protein is an example  
 CC of a first peptide sequence of the invention. The nucleic acid molecules  
 CC are useful in various expression vectors to direct synthesis of the  
 CC corresponding proteins or peptides in a variety of hosts, particularly  
 CC eukaryotic cells, e.g. mammalian or insect cell culture. The nucleic  
 CC acids are also useful for enhancing the immunogenicity of a mammalian  
 CC cell, e.g. tumour cell (sarcoma) or an antigen presenting cell

FT	Domain	/label= Transmembrane_domain 270..288						
FT		/label= Intracellular_domain						
XX								
PN	US6071716-A.							
XX	06-JUN-2000.							
XX	15-NOV-1993;	93US-0153262.						
PF	XX	28-AUG-1991;	91US-0751306.					
PR	XX	01-OCT-1990;	90US-0591300.					
PA	(DAND )	DANA FARBER CANCER INST INC.						
XX	PI	Nadler LM, Freedman GJ, Freedman AS;						
XX	DR	WPI: 2000-422081/36.						
DR	DR-N-PSDB, AAAc1328							
XX	PT	New polynucleotides encoding a B7 activation antigen, useful for regulating T cell mediated immune responses or viral diseases -						
XX	PS	Claim 1; Fig 4; 36pp; English.						
XX	CC	The present sequence is the unique human B cell activation antigen B7 protein. The cDNA encoding this sequence was isolated from a Burkitt lymphoma cell line cDNA library. Selection of cDNA clones was based on expression of B7, as detected by the anti-B7 monoclonal antibody.						
CC	CC	The human B7 cDNA was used in hybridisation analysis to isolate the murine B7 cDNA (see AAA61329). The B7 nucleic acid sequences may be used to generate transgenic, knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The expressed B7 protein is useful for enhancing or blocking activated T cell mediated immune responses and immune function. Modification of B7 expression is useful in the treatment of autoimmune diseases (e.g. rheumatoid arthritis or multiple sclerosis), herpes simplex, influenza, the common cold and HIV. It is also useful in tissue and organ transplantation.						
CC	CC	Sequence 288 AA;	Score 1149; DB 21; Length 288;					
CC	CC	Best Local Similarity 100.0%; Pred. No. 3..4..103; Mismatches 0; Indels 0; Gaps 0;						
CC	CC	Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
CC	CC	Sequence 288 AA;	Score 1149; DB 21; Length 288;					
CC	CC	Best Local Similarity 100.0%; Pred. No. 3..4..103; Mismatches 0; Indels 0; Gaps 0;						
CC	CC	Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
Qy	1	GLSHFCGSVIIHVTKEYKEVATLSCGHNVSVEELAQTRIYQKEKRNVLTMMSGDMMIWP	60	Query	100.0%; Score 1149;	DB 21;	Length 288;	
Db	27	GLSHFCGSVIIHVTKEYKEVATLSCGHNVSVEELAQTRIYQKEKRNVLTMMSGDMMIWP	86	Match	100.0%;	Pred. No. 3..4..103;		
Qy	61	YKNRTIPTDNNSLIVLALRPSDEGTYECVVLKYEDKAFKREHLAEVTLSVKAQDPTPS	120	Local	100.0%;	Matches 216;	Indels 0; Gaps 0;	
Db	87	YKNRTIPTDNNSLIVLALRPSDEGTYECVVLKYEDKAFKREHLAEVTLSVKAQDPTPS	146	Similarity	100.0%;	Conservative	0;	
Qy	121	ISDFEIPTSNRIIICSTSGGPPEPHLWLENGEELNAINTVSDPBTLYAVSSKLDF	180	Matches	216;	Indels 0; Gaps 0;		
Db	147	ISDFEIPTSNRIIICSTSGGPPEPHLWLENGEELNAINTVSDPBTLYAVSSKLDF	206	DB	1 GLSHFCGSVIIHVTKEYKEVATLSCGHNVSVEELAQTRIYQKEKRNVLTMMSGDMMIWP	60		
Qy	161	NMTTNHSFMCILIKYGHLRVNQTFNWNNTKQEHFPDN	216	Qy	27 GLSHFCGSVIIHVTKEYKEVATLSCGHNVSVEELAQTRIYQKEKRNVLTMMSGDMMIWP	86		
Db	207	NMTTNHSFMCILIKYGHLRVNQTFNWNNTKQEHFPDN	242	DB	61 YKNRTIPTDNNSLIVLALRPSDEGTYECVVLKYEDKAFKREHLAEVTLSVKAQDPTPS	120		
Qy	181	NMTTNHSFMCILIKYGHLRVNQTFNWNNTKQEHFPDN	216	Qy	87 YKNRTIPTDNNSLIVLALRPSDEGTYECVVLKYEDKAFKREHLAEVTLSVKAQDPTPS	146		
Db	207	NMTTNHSFMCILIKYGHLRVNQTFNWNNTKQEHFPDN	242	DB	121 ISDFEIPTSNRIIICSTSGGPPEPHLWLENGEELNAINTVSDPBTLYAVSSKLDF	180		
AC	AC	AAV44289;	DB	147 ISDFEIPTSNRIIICSTSGGPPEPHLWLENGEELNAINTVSDPBTLYAVSSKLDF	206			
XX	XX	RESULT 7	Qy	181 NMTTNHSFMCILIKYGHLRVNQTFNWNNTKQEHFPDN	216			
DT	DT	AAV442209 standard; Protein; 288 AA.	DB	207 NMTTNHSFMCILIKYGHLRVNQTFNWNNTKQEHFPDN	242			
XX	XX	29-FEB-2000 (first entry)	AC	AAV54920;				
DB	DB	Human B7.1 co-stimulatory molecule.	XX					

XX 14-FEB-2000 (first entry)  
 XX Human B7.1 protein sequence.  
 XX Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;  
 XX IL-12 p40 subunit; gene therapy; tumour; leukaemia; B7.1 protein.  
 OS Homo sapiens.  
 XX US5994104-A.  
 XX 30-NOV-1999.  
 PD 08-NOV-1996; 96US-0751767.  
 PR 08-NOV-1996; 96US-0751767.  
 XX (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.  
 XX Anderson RJ, Prentice HG, MacDonald ID;  
 XX DR, 2000-038261/03.  
 DR N-PSDB; AAZ40022.  
 XX PT Nucleic acid constructs encoding interleukin-12 fusion proteins useful  
 PT for treating leukemia and other cancers -  
 XX PS Example; Fig 10; 73pp; English.  
 XX CC This sequence represents the human B7.1 protein sequence.  
 CC The invention relates to an isolated nucleic acid construct (I)  
 CC comprising a region encoding an interleukin-12 (IL-12) fusion protein  
 CC (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and a linker  
 CC peptide (joining the subunits)) and a region encoding a B7 protein. (I)  
 CC may be used to produce IL-12 fusion proteins according to standard  
 CC recombinant DNA methodologies. The fusion proteins may be produced either  
 CC in vitro in a fermentation culture or in vivo as part of a gene therapy  
 CC protocol (in this case (I) is used to transform a patients cells, which  
 CC then secrete the functional polypeptide to supplement the patients own  
 CC production of IL-12 or to rectify mutations which lead to the expression  
 CC of inactive polypeptides). The fusion proteins produced in this way may  
 CC be used to treat any disease which responds to IL-12 such as tumours  
 CC (both solid and dispersed of the kidney, breast, colon, ovarian and  
 CC cervical tumours and melanomas) and in particular, tumours of the blood  
 CC such as leukaemia. Alternatively, the polypeptides may be used as  
 CC antigens in the production of antibodies to IL-12 and to assay for  
 CC agonists and antagonists of its activity. The antibody and antagonists  
 CC may also be used to inhibit the activity of IL-12. (I) may also be used  
 CC diagnostically as a probe which hybridizes to sequences encoding IL-12  
 CC and the antibodies may be used to detect the presence of IL-12  
 CC polypeptides in samples. They may be used diagnostically to quantitate  
 CC the expression of the polypeptide by patients, and hence which subjects  
 CC may be in need of restorative therapy.  
 XX Sequence 288 AA;  
 SQ Query Match 100.0%; Score 1149; DB 21; Length 288;  
 Best Local Similarity 100.0%; Prod. No. 3.4e-103;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 27 GLSHFCGIVTHVKVEVATLSCGHNVSEELAQTRIYWERKEKKMVLTMMMSGDMNIWPE 86  
 YY 61 YKNRTIDITNNLSTIVLALRPSDEGTYCCVVLKYEDAFKREHAAETVLSYKADFPTPS 120  
 DB 87 YKNRTIDITNNLSTIVLALRPSDGTYCCVVLKYEDAFKREHAAETVLSYKADFPTPS 146  
 YY 121 ISDPEIPTSNIRRICSTSGGFPEPHLSENGEELNANTVSDPPTELYAVSSKDF 180  
 DB 147 ISDPEIPTSNIRRICSTSGGFPEPHLSENGEELNANTVSDPPTELYAVSSKDF 206  
 YY Query Match 100.0%; Score 1149; DB 22; Length 288;  
 Best Local Similarity 100.0%; Prod. No. 3.4e-103;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 GLSHFCGIVTHVKVEVATLSCGHNVSEELAQTRIYWERKEKKMVLTMMMSGDMNIWPE 60  
 YY 27 GLSHFCGIVTHVKVEVATLSCGHNVSEELAQTRIYWERKEKKMVLTMMMSGDMNIWPE 86  
 YY 61 YKNRTIDITNNLSTIVLALRPSDEGTYCCVVLKYEDAFKREHAAETVLSYKADFPTPS 120  
 YY 87 YKNRTIDITNNLSTIVLALRPSDGTYCCVVLKYEDAFKREHAAETVLSYKADFPTPS 146  
 YY 121 ISDPEIPTSNIRRICSTSGGFPEPHLSENGEELNANTVSDPPTELYAVSSKDF 180  
 YY 147 ISDPEIPTSNIRRICSTSGGFPEPHLSENGEELNANTVSDPPTELYAVSSKDF 206  
 YY Query Match 100.0%; Score 1149; DB 22; Length 288;

Db	87	YKRTTIFDTNNLISVIALRPSDGTYECVVLKERRQHABVTLSVKADDPTPS	146
Qy	121	ISDFEIPTSNIRRITCSTSGGFPEPHLSNLLENGEELNAINNTVSQDPETELYAVSSKLD	180
Db	147	ISDEIPTSNIRRITCSTSGGFPEPHLSNLLENGEELNAINNTVSQDPETELYAVSSKLD	206
Qy	181	NMPTTNHSFMCLIKYGHLYRNQTFNWNTTQEHFPDN	216
Db	207	NMPTTNHSFMCLIKYGHLYRNQTFNWNTTQEHFPDN	242
RESULT 10			
AAB19959	ID	AAB19959 standard; Protein; 288 AA.	
XX	XX		
AC	AC		
XX	XX		
DT	19-MAR-2001	(first entry)	
XX	XX		
DE	Human B lymphocyte antigen B7.		
XX			
KW	Human; B7; B lymphocyte; antigen; T cell costimulatory molecule;		
KW	CD28; CTLA4; tumour; melanoma; neuroblastoma; leukaemia; carcinoma;		
KW	metastasis; antitumour; therapy.		
XX			
OS	Homo sapiens.		
XX			
Key		Location/Qualifiers	
Peptide		1..34	
FT		/label= Signal_peptide	
FT		35..288	
Protein		/label= Mature_protein	
FT		35..242	
Domain		/note= "extracellular domain"	
FT		243..269	
Domain		/note= "transmembrane domain"	
FT		270..288	
Domain		/note= "intracellular domain"	
FT		35..138	
Domain		/note= "immunoglobulin V-set domain"	
FT		139..236	
Domain		/note= "immunoglobulin C-set domain"	
FT		53..55	
Modified-site		/note= "Asn is N-glycosylated"	
FT		89..91	
Modified-site		/note= "Asn is N-glycosylated"	
FT		98..100	
Modified-site		/note= "Asn is N-glycosylated"	
FT		186..188	
Modified-site		/note= "Asn is N-glycosylated"	
FT		207..209	
Modified-site		/note= "Asn is N-glycosylated"	
FT		211..213	
Modified-site		/note= "Asn is N-glycosylated"	
FT		226..228	
Modified-site		/note= "Asn is N-glycosylated"	
FT		232..234	
Modified-site		/note= "Asn is N-glycosylated"	

PI	Nadier LM;
XX	WPI: 2001-079388/09.
DR	DR N-PSDB; AAA89224.
XX	Modifying tumor cell inhibiting recurrence transfecting tumor ce
XX	Claim 4; Column 31-33
PT	PT
PT	PT
XX	PS
XX	CC
CC	The present sequence cell costimulatory molecule cells modified to express especially B7, are directed transfection with a recombinant molecule, by using an antibody of the T cell costimulatory by coupling the T cell surface. Tumour cells histocompatibility molecule or in which expression chain, is inhibited are used to treat a patient metastatic spread or melanoma, a neuroblastoma specifically inducing method for treating a are also disclosed. of the tumour cell in response is effective unmodified tumour ce Thus, the effector cell modified tumour cell costimulatory molecule
XX	Sequence 288 AA;
SQ	Query Match Best Local Similarity Matches 216; Conserva
Qy	1 GLSHFCGVITH
Db	27 GLSHFCGVITH
Qy	61 YKNTIIFTDTNN
Db	87 YKNTIIFTDTNN
Qy	121 ISDEEIPSNIIL
Db	147 ISDEEIPSNIIL
Qy	181 NMITINHSFMCLL
Db	207 NMITINHSFMCLL

ABP68580-11	ABP68580	standard	protein; 288 AA.
ABP68580	ID	ABP68580	
XX	XX		
XX	AC		
XX	AC		
DT	DT		
XX	XX		
DE	DE		
			Novel co-stimulatory molecule (NCSM) Protein SEQ ID NO:278.
			Novel co-stimulatory molecule; NCSM; CD28; binding; CTLA-4 receptor; CD28 receptor; CTLA-4; gene therapy; vaccine; immunosuppressive; HIV; neuroprotective; antiarthritic; dermatological; anti-HIV; anti-fungal; antiviral; antinflammatory; antiangiogenic; antiarrhythmic; convulsive; virucide.
			08-JAN-2003 (first entry)

KW antibacterial; immunostimulant; T cell response; immune response; tumour;  
 KW autoimmune disorder; multiple sclerosis; rheumatoid arthritis; psoriasis;  
 KW lupus erythematosus; type I diabetes; cancer; viral infection;  
 KW bacterial infection.

OS Homo sapiens.

XX WO200200717-A2.

XX PD 03-JAN-2002.

XX PF 22-JUN-2001; 2001WO-US19973.

XX PR 23-JUN-2000; 2000US-213945P.

XX PR 17-OCT-2000; 2000US-241245P.

XX PA (MAXY-) MAXYGEN INC..

XX PI Punnonen J, Lazetic ALL, Leong SR, Chang CJ, Apt D, Gustafsson C;

XX DR WPI; 2002-583387/62.

XX X Novel co-stimulatory molecule nucleic acids and polypeptides, useful

PT for treating e.g. autoimmune disorder, cancer, viral or bacterial

PT infection, comprises greater CD28/CTLA-4 binding affinity ratio than

PT binding affinity ratio of human B7-1

XX PS Claim 80; Page 280; 364pp; English.

XX CC The present invention describes an isolated or recombinant novel

CC co-stimulatory molecule (NSCM) nucleic acid (I) and NSCM proteins

CC (II) can have immunosuppressive, neuroprotective, antirheumatic,

CC antiarthritic, dermatological, antiinflammatory, antipsoriatic, virucide,

CC antidiabetic, cytotoxic, anti-HIV, antibacterial and immunostimulant

CC activities. They can be used in gene therapy, antisense therapy and

CC vaccine production, and as CD28 and CTLA-4 modulators. (II) is useful for

CC inducing, inhibiting and modifying T-cell proliferation and modifying

CC T-cell activation in culture. (I) is useful for modulating or altering a

CC T-cell response specific to an antigen (e.g. antigen of an infectious

CC agent or cancer) in a subject, where (I) interacts with or binds to a T

CC cell surface receptor to enhance T-cell response so that cells bearing

CC the antigen are eliminated or to suppress or inhibit T-cell response.

CC Alternatively (I) is introduced into cells of a tumour. (I) and (II) are

CC useful for the therapeutic or prophylactic treatment of a disease or

CC disorder in a human, where an immune response induced by the immunogen is

CC enhanced, diminished or modified in vivo, in vitro or ex vivo

CC administration of (I) or (II) to the cells of the subject. In particular

CC disease that may be treated using (I) and (II) are autoimmune disorders,

CC multiple sclerosis, rheumatoid arthritis, lupus erythematosus, psoriasis,

CC type I diabetes, allogeneic xenogeneic grafts or transplants, cancer,

CC viral infections (e.g. HIV) or bacterial infection. ABP6436 to ABP68443

CC and ABV9478 to ABV9485 represent sequences used in the exemplification

CC of the present invention. ABV94486 to ABV94627 and ABP68444 to ABP8595

CC represent NSCM sequences from the present invention.

XX Sequence 288 AA;

XX Query Match 100.0%; Score 1149; DB 23; Length 288;

XX Best Local Similarity 100.0%; Prod. No. 3..e-103;

XX Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ

XX

XX

XX

XX

QY 181 NMNTNHSPMCLIKYGHLRVNQTFNWNNTTKQEHFPDN 216  
 QY 207 NMNTNHSPMCLIKYGHLRVNQTFNWNNTTKQEHFPDN 242

Db RESULT 1.2

Db ABB78363 standard; Protein; 288 AA.

Db XX ID ABB78363;

Db XX AC ABB78363;

Db XX DT 16-DEC-2002 (first entry)

Db XX DE Amino acid sequence of human B7-1 (CD80).

Db XX KW B7 protein; B7-1; CD80; CD28 ligand; T cell; T cell proliferation;

Db XX KW infectious disease; cancer; immunotherapy; immunotherapy.

Db XX Homo sapiens.

Db XX OS Homo sapiens.

Db XX PN US2002115214-A1.

Db XX PR 22-AUG-2002.

Db XX PR 26-JAN-1996; 96US-0592711.

Db XX PR 23-NOV-1988; 88US-0275433.

Db XX PR 04-MAY-1995; 92US-0864805.

Db XX PR 07-APR-1992; 92US-0864807.

Db XX PR 07-APR-1992; 92US-0864866.

Db XX PR 04-JUN-1993; 93US-0073223.

Db XX PR 03-JUN-1994; 94US-0253954.

Db XX PR 10-MAR-1995; 95US-0403253.

Db XX PR 04-MAY-1995; 95US-0435816.

Db XX PA (JUNE/) JUNE C H. (JUNE/)

Db XX PA (THOMSON C B. THOMPSON C B.

Db XX PA (NABEL G J. NABEL G J.

Db XX PA (GRAY G S. GRAY G S.

Db XX PA (RENNER P D. RENNERT P D.

Db XX PA (DR DR WPI; 2002-712476/77.

Db XX PA June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;

Db XX PR WPI; 2002-712476/77.

Db XX PR DR N-PSDB; ABV7339.

Db XX PR Disclosure; Page 40-41; 88pp; English.

Db XX CC The present sequence is a member of the B7 family of protein, B7-1

Db XX CC (CD80). B7 proteins are ligands for CD28. Activated T cells are contacted

Db XX CC with a stimulatory form of a natural ligand for CD28, such as a B7

Db XX CC protein, for costimulation. B7 molecules are used in the method of the

Db XX CC invention. The method involves activating a population of the

Db XX CC of T cells to proliferate. The method involves activating population of

Db XX CC T cells, stimulating an accessory molecule (e.g. CD28) on T cell surface

Db XX CC with a ligand (e.g. B7 protein) which binds the molecule, to induce

Db XX CC proliferation of T cells, monitoring proliferation of T cells in response

Db XX CC to continuing exposure to the ligand, and reactivating and restimulating

Db XX CC T cells when rate of proliferation of the cells. The method is useful for inducing further

Db XX CC proliferation of T cells. The method is useful for inducing

Db XX CC proliferation of T cells, for use in treatment of infectious disease,

Db XX CC cancer and immunotherapy. The method allows for the expansion of a

Db XX CC population of T cells in numbers sufficient to reconstitute an

Db XX CC individual's total CD4+ or CD8+ T cell population. The resulting T cell

Db XX CC population can be genetically engineered and used for immunotherapy or

Db XX CC can be used in methods of in vitro analyses of infectious agents. A

Db XX CC population of tumour-infiltrating lymphocytes can be obtained from an

Db XX CC individual afflicted with cancer and the T cells stimulated to

QY 1 GLSHFCGIVHVTKEVATLSQHNVSEELAQTRVWQKRVMTTMMGSDMNTWPE 60  
 QY 27 GLSHFCGIVHVTKEVATLSQHNVSEELAQTRVWQKRVMTTMMGSDMNTWPE 86

Db 61 YKNTTIDTNNLSVILALRPSDEGTVBCVILYKEKAFKREHLAETVLSVYKADFPPTS 120

Db 87 YKNTTIDTNNLSVILALRPSDEGTVBCVILYKEKAFKREHLAETVLSVYKADFPPTS 146

QY 121 ISDFEIPTSNIRRICSTSGGFPEPHLSWLENGBELNAINTVSQDPETELYAVSSKIDF 180

Db 147 ISDFEIPTSNIRRICSTSGGFPEPHLSWLENGBELNAINTVSQDPETELYAVSSKIDF 206

CC proliferate to sufficient numbers. The resulting T cell population can be genetically transduced to express tumour necrosis factor (TNF) or other factor and restored to the individual. CD4+ T cells expanded by this method are useful in the treatment of HIV infection in an individual.

XX \*SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;  
Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Sequence 288 AA;

```

Qy 1 GLSHFCSGVIVHTKEYKEVATLSCGHNVSEELAQTRIYQKEKRVLTMSGDNNTIWE 60
Db 27 GLSHFCSGVIVHTKEYKEVATLSCGHNVSEELAQTRIYQKEKRVLTMSGDNNTIWE 86
Qy 61 YKNRTIIFDTNNLSIVIALRPSDEGTYECVVLKYERDAFKREHLaETVLSVKADEPFTPS 120
Db 87 YKNRTIIFDTNNLSIVIALRPSDEGTYECVVLKYERDAFKREHLaETVLSVKADEPFTPS 146
Qy 121 ISDFEIPSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTVSQDDETELAVASSKLDF 180
Db 147 ISDFEIPSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTVSQDDETELAVASSKLDF 206
Qy 181 NMTTNHSFMCMLIKYGHLRVNOTFNWNTTKQEHFPDN 216
Db 207 NMTTNHSFMCMLIKYGHLRVNOTFNWNTTKQEHFPDN 242

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RESULT 13

AP015800 standard; Protein; 288 AA.  
XX ID AAO15800 standard; Protein; 288 AA.

AC AC015800;  
XX DT 05-DEC-2002 (first entry)  
DE Human B7-1 protein.

XX Human; Gene therapy; B7-like protein; Graft vs host disease; immune response modulation; T-lymphocyte-related disorder; asthma; allergy; allergic rhinitis; psoriasis; chronic inflammatory disease; autoimmune disease; graft rejection; neoplasia; viral infection; HIV; herpes; bone disorder; B7 lymphoma; carcinoma; T-cell leukaemia.  
XX Homo sapiens.

OS XX US200206730-A1.  
PN XX 08-AUG-2002.

XX PF 26-JUL-2001; 2001US-0910174.  
XX PR 20-JUL-2000; 2000US-0920461.  
XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Coyle AJ, Fraser CC, Manning S;  
XX WPI: 2002-712398/77.

XX Novel human B-7-like polypeptide referred to as B7-H2, useful for identifying a compound which modulates activity of the polypeptide, and treating T-lymphocyte-related, immune and bone disorders - Disclosure; Fig 1; 101pp; English.

XX The invention comprises the amino acid and coding sequences of B7-like proteins; The B7-like proteins/nucleic acids of the invention are useful for modulating immune responses and for diagnosing and treating disorders that involve B7-like protein activity or nucleic acid expression. Such disorders include T-lymphocyte-related disorders; asthma; allergies (e.g. allergic rhinitis); psoriasis; chronic inflammatory diseases;

CC autoimmune diseases; graft rejection; graft vs host disease; neoplasia; viral infections (e.g. HIV and herpes); bone disorders; B7 lymphomas; carcinomas; and T-cell leukaemias. The present amino acid sequence represents a human B7-like protein.

XX SQ Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

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Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

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Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

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Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;<br

PS Disclosure; Page 17-18; 25pp; English.

XX The invention relates to a tumour cell which is modified to express a T cell costimulatory molecule. Also included is a method of treating a subject with a tumour, by obtaining tumour cells and T lymphocytes from the subject, culturing the T lymphocytes from the subject in vitro with the tumour cells from the subject and with a stimulatory form of a T cell costimulatory molecule and administering the T lymphocyte to the subject. The tumour cell is useful for treating cancer including sarcoma, lymphoma, leukaemia, carcinoma, neuroblastoma, melanoma, by obtaining tumour cells from the subject, modifying the tumour cells to express a T cell costimulatory molecule and administering the tumour cells to the subject. The cell is also useful for preventing or treating metastatic spread of a tumour or preventing or treating recurrence of a tumour in a subject, and for inducing an anti-tumour response by CD4+ T helper lymphocytes in a subject with a tumour. As the effector phase of the T cell-mediated immune response is not dependent upon expression of a costimulatory molecule by tumour cells, the T cell-mediated immune response generated by administration of a modified tumour cell is effective against not only the modified tumour cells but also the unmodified tumour cells from which they were derived. The present sequence represents a T cell costimulatory molecule, B cell activation antigen B7, the human gene for which is located on chromosome 3.

XX Sequence 288 AA;

Query Match 100.0%; Score 1149; DB 23; Length 288;

Best Local Similarity 100.0%; Pred. No. 3.4e-103; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCSGVIVHTKEYEATLSCGHNSVVEELAQTRIYQKEKRMVLTMSGDMNINPE 60  
Db 27 GLSHFCSGVIVHTKEYEATLSCGHNSVVEELAQTRIYQKEKRMVLTMSGDMNINPE 86  
Qy 61 YKNRTIPTDITNNLSIVLALRPSDETYECVVLKYKEKRMVLTLSVKAQTRIYQKEKRMVLTMSGDMNINPE 120  
Db 87 YKNRTIPTDITNNLSIVLALRPSDETYECVVLKYKEKRMVLTLSVKAQTRIYQKEKRMVLTMSGDMNINPE 146  
Qy 121 ISDFFEPTSNRRICTSGCFPEPHLSMLENGEELNANTVQDPEPELYAVSSKDF 180  
Db 147 ISDFFEPTSNRRICTSGCFPEPHLSMLENGEELNANTVQDPEPELYAVSSKDF 206  
Qy 181 NMTTNHSFMCUJKYGHLYRNQTFNNTKOBHFDPN 216  
Db 207 NMTTNHSFMCUJKYGHLYRNQTFNNTKOBHFDPN 242

FT Modified-site /note= "Asn is N-glycosylated" 89..91  
FT Modified-site /note= "Asn is N-glycosylated" 98..100  
FT Domain /note= "Asn is N-glycosylated" 139..236  
FT Modified-site /note= "Ig C-set domain" 186..188  
FT Modified-site /note= "Asn is N-glycosylated" 207..209  
FT Domain /note= "Asn is N-glycosylated" 211..213  
FT Modified-site /note= "Asn is N-glycosylated" 226..228  
FT Modified-site /note= "Asn is N-glycosylated" 232..234  
FT Domain /note= "Asn is N-glycosylated" 243..269  
FT Domain /label= Transmembrane\_domain 270..288  
FT Domain /label= Intracellular\_domain XX US352694-B1.  
PN XX  
SQ XX  
PP 05 MAR 2002.  
XX 05-MAR-1995; 95US-0403253.  
XX 10-MAR-1995; 95US-0403253.  
PR 03-JUN-1994; 94US-0253964.  
PA (GEMY ) GENETICS INST INC.  
PA (UMMI ) UNIV MICHIGAN.  
PI June CH, Thompson CB, Nabel GJ, Gray GS, Rennert PD;  
XX DR WPI: 2002-314696/35.  
DR N-PSDB; AAD27967.  
XX  
PT Inducing T cell population to proliferate, useful in cancer therapy, comprises activating T cells by contacting T cells in vitro with immobilized anti-CD3 antibody and stimulating accessory molecule on T cell surface  
PT  
PT  
PT  
PT  
PT  
PS Example 11; Column 59-62; 71pp; English.  
XX  
CC The invention relates to a method of inducing T cell population to proliferate for use in therapy comprising activating T cells by contacting T cells in vitro with anti-CD3 antibody which is immobilised on solid phase surface, and stimulating accessory molecule on T cell surface in vitro with anti-CD28 antibody, or stimulatory form of natural ligand for CD28 such as B7-1 or B7-2. The method is useful for inducing a population of T cells to proliferate in sufficient numbers for use in therapy e.g., for treating cancer or an infectious disease. The method can be used to selectively expand the population of CD28+, CD4+, CD8+, CD28R0+ or CD28R0+ T cells for immunotherapy. The T cell population resulting by the method can be genetically transduced and used for immunotherapy or can be used for in vitro analysis of infectious agents such as human immunodeficiency virus (HIV). Proliferation of a population of CD4+ T cells obtained from an individual infected with HIV can be achieved and the cells rendered resistant to HIV infection. Following the expansion of the T cells to sufficient numbers, the expanded T cells are restored to the individual. Also CD4+ T cells expanded by the above mentioned is useful for treating HIV infection in an individual. A population of tumour-infiltrating lymphocytes can be obtained from an individual afflicted with cancer and the T cells stimulated to proliferate to sufficient numbers and restored to the individual. The supernatants from cultures of T cells expanded from above mentioned method are useful as a rich source of cytokines and can be used to sustain T cells in vivo or ex vivo. Stimulating and expanding a population of antigen specific T cells are useful in therapeutic conditions where it is desirable to upregulate an immune response. The T cell proliferation occurs in the absence of exogenous growth factors or accessory cells. The present

RESULT 15

AAE14633 standard; Protein; 288 AA.

XX AC AAE14633;

XX DT 16-JUL-2002 (first entry)

XX DB Human B7-1 protein.

XX KW T cell; CD3; accessory molecule; CD28; cancer; infectious disease; KW immunotherapy; human immunodeficiency virus; HIV infection; KW cytokine; human; B7-1; CD80.

XX OS Homo sapiens.

XX FH Key

Peptide 1..34 /label= Signal\_peptide

PT Protein 35..288 /note= "Mature B7-1 protein"

PT Domain 35..242 /label= Extracellular\_domain

PT Domain 35..138 /note= "Ig V-set domain"

PT Modified-site 53..55 /note= "Ig V-set domain"

CC sequence is human B7-1 (CD80) transmembrane protein used in the invention.

CC	Sequence	288 AA;
XX	Sequence	288 AA;
Query Match	100.0%;	Score 1149; DB 23; Length 288;
Best Local Similarity	100.0%;	Pred. No. 3.4e-103;
Matches	216;	Conservative 0; Mismatches 0; Indels 0;
Qy	1	GLSHFCGVIVHTKEYKEVATLSCGHNSVVELAQTRIYQEKVKVLTMSGDNIWPE 60
Db	27	GLSHFCGVIVHTKEYKEVATLSCGHNSVVELAQTRIYQEKVKVLTMSGDNIWPE 86
Qy	61	YKNRTIFIDITNNLSIVLALRPSDEGTYECVVKYKEVDAFKREHLLAEVTLSVKADPPTPS 120
Db	87	YKNRTIFIDITNNLSIVLALRPSDEGTYECVVKYKEVDAFKREHLLAEVTLSVKADPPTPS 146
Qy	121	ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTVSDQDPETELYAVSSKLDF 180
Db	147	ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTVSDQDPETELYAVSSKLDF 206
Qy	181	NMTTNHSFMCLIKYGLRVNQTFNNNTTKQEHFPDN 216
Db	207	NMTTNHSFMCLIKYGLRVNQTFNNNTTKQEHFPDN 242

## RESULT 16

AAE15829 standard; Protein; 288 AA.

XX

AAE15829;

XX

DT 26-MAR-2002 (first entry)

XX

Human co-stimulatory molecule, B7-1 protein.

XX Human; vaccine; immunostimulatory molecule; interferon; IFN; therapy; antigen; presentation; vaccine; tumourgenesis; cancer; cytostatic; antitumour; antibacterial; fungicide; protozoicide; B7-1.

XX Homo sapiens.

XX

PN WO200188097-A1.

XX

PD 22-NOV-2001.

XX

PP 17-MAY-2001; 2001WO-AU00565.

XX

PR 17-MAY-2000; 2000AU-0007553.

XX

PA, (MONU ) UNIV MONASH.

XX

PT Ralph SJ;

XX

DR WPI; 2002-0822990/11.

XX

DR N-PSDB, AA255509.

XX

PT New composition, useful for treatment and/or prophylaxis of cancer and tumor, comprises immunostimulatory molecule and animal cells cultured in presence of interferon to enhance antigen presenting function of the cells -

XX

PS Claim 6; Page 99-100; 127bp; English.

XX

PT The present invention relates to a composition of matter comprising an immunostimulatory molecule and animal cells cultured in the presence of at least one interferon (IFN) for a time and under conditions sufficient to enhance the antigen presenting function of the cells. The invention is used as vaccine. The composition is useful for treatment and/or prophylaxis of tumourgenesis, cancer, viral, bacterial, fungal and protozoal infections. The composition which comprises the soluble immunostimulatory molecule and the cultured animal cells is administered separately, sequentially or simultaneously to the patient. The present

CC sequence is human co-stimulatory molecule, B7-1 protein.

CC	Sequence	288 AA;
XX	Sequence	288 AA;
Query Match	100.0%;	Score 1149; DB 23; Length 288;
Best Local Similarity	100.0%;	Pred. No. 3.4e-103;
Matches	216;	Conservative 0; Mismatches 0; Indels 0;
Qy	1	GLSHFCGVIVHTKEYKEVATLSCGHNSVVELAQTRIYQEKVKVLTMSGDNIWPE 60
Db	27	GLSHFCGVIVHTKEYKEVATLSCGHNSVVELAQTRIYQEKVKVLTMSGDNIWPE 86
Qy	61	YKNRTIFIDITNNLSIVLALRPSDEGTYECVVKYKEVDAFKREHLLAEVTLSVKADPPTPS 120
Db	87	YKNRTIFIDITNNLSIVLALRPSDEGTYECVVKYKEVDAFKREHLLAEVTLSVKADPPTPS 146
Qy	121	ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTVSDQDPETELYAVSSKLDF 180
Db	147	ISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTVSDQDPETELYAVSSKLDF 206
Qy	181	NMTTNHSFMCLIKYGLRVNQTFNNNTTKQEHFPDN 216
Db	207	NMTTNHSFMCLIKYGLRVNQTFNNNTTKQEHFPDN 242

## RESULT 17

AAM50795 standard; Protein; 288 AA.

ID	Location/Qualifiers
AAM50795;	XX
AC	XX
XX	XX
DT 23-APR-2002 (first entry)	XX
DE Human B-lymphocyte antigen B7.	XX
XX B-lymphocyte antigen B7; human; T-cell costimulatory molecule; tumour; sarcoma; lymphoma; melanoma; neuroblastoma; leukaemia; carcinoma; cancer; metastasis; gene therapy.	XX
XX Homo sapiens.	OS
XX	XX
PH Key	XX
FT Peptide	XX
FT Protein	XX
FT /label= Mature_protein	35..288
FT Domain	35..242
FT Domain	243..269
FT Domain	270..288
FT Domain	35..138
FT /label= Ig_V-set_domain	139..236
FT Domain	139..236
FT /label= Ig_C-set_domain	53..55
FT Modified-site	53..188
FT Modified-site	207..209
FT Modified-site	211..213
FT Modified-site	226..228
FT Modified-site	232..234
FT Modified-site	XX



Qy	121	ISDPEIPTSNIRRRIICSTSGFPPEPHISWLNGEELNAINTTVSQDPETELYAVSSKLDF	180	SQ	Sequence	288 AA;
Db	147	ISDPEIPTSNIRRRIICSTSGFPPEPHISWLNGEELNAINTTVSQDPETELYAVSSKLDF	206		Query Match	100.0% ; Score 1149; DB 24;
Qy	181	NMTTNHSFMCILIKYGHLRVNQTFNNNTTKQEHFPDN	216		Best Local Similarity	100.0% ; Pred. No. 3 4e-103;
-Db	207	NMTTNHSFMCILIKYGHLRVNQTFNNNTTKQEHFPDN	242		Matches	216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	RESULT 19					
	ABU07247	Human expressed protein tag (EPT) #1948.				
	ID	ABU07247 standard; Protein; 288 AA.				
	XX					
	AC	ABU07247;				
	XX	29-JAN-2003 (first entry)				
	DT					
	DE	Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.				
	XX					
	OS	Homo sapiens.				
	XX					
	PN	WO200278524-A2.				
	XX					
	PD	10-OCT-2002.				
	XX					
	PF	28-MAR-2002; 2002WO-US09671.				
	XX					
	PR	28-MAR-2001; 2001US-279495P.				
	PR	21-MAY-2001; 2001US-392544P.				
	PR	08-AUG-2001; 2001US-310801P.				
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	PR	04-DEC-2001; 2001US-336780P.				
	PR	20-FEB-2002; 2002US-358985P.				
	XX					
	PA	(ZYCO-) ZYCO'S INC.				
	XX					
	PI	Chicz RM, Tomlinson AJ, Urban RG;				
	XX					
	WPI:	2003-040607/03.				
	DR					
	XX					
	PF	28-MAR-2002; 2002WO-US09671.				
	XX					
	PR	28-MAR-2001; 2001US-279495P.				
	PR	21-MAY-2001; 2001US-292544P.				
	PR	08-AUG-2001; 2001US-310801P.				
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	PF	28-MAR-2002; 2002WO-US09671.				
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	PR	28-MAR-2001; 2001US-279495P.				
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	PR	21-MAY-2001; 2001US-292544P.				
	PR	08-AUG-2001; 2001US-310801P.				
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	PR	21-MAY-2001; 2001US-292544P.				
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	PR	21-MAY-2001; 2001US-292544P.				
	PR	08-AUG-2001; 2001US-310801P.				
	PR	01-OCT-2001; 2001US-326370P.				
	PR	04-DEC-2001; 2001US-336780P.				
	PR	20-FEB-2002; 2002US-358985P.				
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	PF	28-MAR-2002; 2002WO-US09671.				
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	PR	28-MAR-2001; 2001US-279495P.				
	PR	21-MAY-2001; 2001US-292544P.				
	PR	08-AUG-2001; 2001US-310801P.				
	PR	01-OCT-2001; 2001US-326370P.				
	PR	04-DEC-2001; 2001US-336780P.				
	PR	20-FEB-2002; 2002US-358985P.				
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	PR	21-MAY-2001; 2001US-292544P.				
	PR	08-AUG-2001; 2001US-310801P.				
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	PA	(ZYCO-) ZYCO'S INC.				
	XX					
	PI	Chicz RM, Tomlinson AJ, Urban RG;				
	XX					
	WPI:	2003-040607/03.				
	DR					
	XX					
	PF	28-MAR-2002; 2002WO-US09671.				
	XX					
	PR	28-MAR-2001; 2001US-279495P.				
	PR	21-MAY-2001; 2001US-292544P.				
	PR	08-AUG-2001; 2001US-310801P.				
	PR	01-OCT-2001; 2001US-326370P.				
	PR	04-DEC-2001; 2001US-336780P.				
	PR	20-FEB-2002; 2002US-358985P.				
	XX					
	PA	(ZYCO-) ZYCO'S INC.				
	XX					
	PI	Chicz RM, Tomlinson AJ, Urban RG;				
	XX					
	WPI:	2003-040607/03.				
	DR					
	XX					
	PF	28-MAR-2002; 2002WO-US09671.				
	XX					
	PR	28-MAR-2001; 2001US-279495P.				
	PR	21-MAY-2001; 2001US-292544P.				
	PR	08-AUG-2001; 2001US-310801P.				
	PR	01-OCT-2001; 2001US-326370P.				
	PR	04-DEC-2001; 2001US-336780P.				
	PR	20-FEB-2002; 2002US-358985P.				
	XX					

CC polypeptide. The purified polypeptide, or the antibody that binds to  
 CC this polypeptide, is useful for treating cancer. The polypeptide is  
 CC also useful for identifying compounds that binds to a naturally  
 CC processed class I or class II MHC-binding polypeptide. The polypeptides  
 CC and polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. There are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling.

CC Note: This sequence does not appear in the printed specification but was  
 CC obtained in electronic format directly from WIPO at  
 CC [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).

XX Sequence 288 AA:

Query Match 100.0%; Score 1149; DB 24; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 216; Conservative 0; Nismatches 0; Gaps 0;

Qy 1 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 60  
 Db 27 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 86

Qy 61 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 120  
 Db 87 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 146

Qy 121 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 180  
 Db 147 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 206

Qy 181 NMTTNHSFMCMLIKYGHLRNQTFNNTQEHFPDN 216  
 Db 207 NMTTNHSFMCMLIKYGHLRNQTFNNTQEHFPDN 242

## RESULT 21

ABU07249

ID ABU07249 standard; Protein; 288 AA.

XX AC ABU07249;

XX DT 29-JAN-2003 (First entry)

XX DB Human expressed protein tag (EPT) #1950.

XX Translational profiling; expressed protein tag; EPT; kinase;  
 KW phosphatase; protease; protease inhibitor; transporter;  
 KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer;  
 KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;  
 KW leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US09671.

XX PR 28-MAR-2001; 2001US-279495.

PR 21-MAY-2001; 2001US-292544.

PR 08-AUG-2001; 2001US-310801.

PR 04-DEC-2001; 2001US-326370.

PR 20-FEB-2002; 2002US-358385P.

PA (ZYCO) ZYCO INC.

XX PI Chicz RM, Tomlinson AJ, Urban RG;

XX

DR WPT; 2003-040607/03.

XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters, PT  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma  
 PT or leukemia -

XX

Example 2: SEQ ID No 1950; 134PP; English.

XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor.  
 CC The polypeptide is useful as an immunogenic composition for eliciting  
 CC in a mammal an immunogenic response directed against any of the purified  
 CC polypeptide. The purified polypeptide, or the antibody that binds to  
 CC this polypeptide, is useful for treating cancer. The polypeptide is  
 CC also useful for identifying compounds that binds to a naturally  
 CC processed class I or class II MHC-binding polypeptide. The polypeptides  
 CC and polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling.

CC Note: This sequence does not appear in the printed specification but was  
 CC obtained in electronic format directly from WIPO at  
 CC [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).

XX Sequence 288 AA:

Query Match 100.0%; Score 1149; DB 24; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 216; Conservative 0; Nismatches 0; Gaps 0;

Qy 1 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 60  
 Db 27 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 86

Qy 61 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 120  
 Db 87 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 146

Qy 121 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 180  
 Db 147 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 206

Qy 181 NMTTNHSFMCMLIKYGHLRNQTFNNTQEHFPDN 216  
 Db 207 NMTTNHSFMCMLIKYGHLRNQTFNNTQEHFPDN 242

SQ Sequence 288 AA:

Query Match 100.0%; Score 1149; DB 24; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 216; Conservative 0; Nismatches 0; Gaps 0;

Qy 1 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 60  
 Db 27 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 86

Qy 61 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 120  
 Db 87 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 146

Qy 121 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 180  
 Db 147 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 206

SQ Sequence 288 AA:

Query Match 100.0%; Score 1149; DB 24; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 216; Conservative 0; Nismatches 0; Gaps 0;

Qy 1 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 60  
 Db 27 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 86

Qy 61 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 120  
 Db 87 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 146

Qy 121 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 180  
 Db 147 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 206

SQ Sequence 288 AA:

Query Match 100.0%; Score 1149; DB 24; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 216; Conservative 0; Nismatches 0; Gaps 0;

Qy 1 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 60  
 Db 27 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 86

Qy 61 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 120  
 Db 87 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 146

Qy 121 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 180  
 Db 147 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 206

SQ Sequence 288 AA:

Query Match 100.0%; Score 1149; DB 24; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 216; Conservative 0; Nismatches 0; Gaps 0;

Qy 1 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 60  
 Db 27 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 86

Qy 61 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 120  
 Db 87 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 146

Qy 121 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 180  
 Db 147 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 206

SQ Sequence 288 AA:

Query Match 100.0%; Score 1149; DB 24; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 216; Conservative 0; Nismatches 0; Gaps 0;

Qy 1 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 60  
 Db 27 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 86

Qy 61 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 120  
 Db 87 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 146

Qy 121 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 180  
 Db 147 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 206

SQ Sequence 288 AA:

Query Match 100.0%; Score 1149; DB 24; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 216; Conservative 0; Nismatches 0; Gaps 0;

Qy 1 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 60  
 Db 27 GLSHFCGVIVHVTKEYEATLSCGHNVSVELAOTRIVQEKERKVMVLTMSGDMNTIPE 86

Qy 61 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 120  
 Db 87 YKNRTIPTDITNNLSIVIALRPSDGTYECVVLKYEKDAFKREHLAETVLSVKADEPPPS 146

Qy 121 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 180  
 Db 147 ISDFEITPSNIRRICSTSGGGFPEPHLWLENGEELNAINTVSQDPETELYAVSSKLD 206

SQ Sequence 288 AA:

OS Homo sapiens.

XX

ID ABU07250 standard; Protein; 288 AA.

XX AC ABU07250;

XX DT 29-JAN-2003 (First entry)

DE Human expressed protein tag (EPT) #1951.

XX KW Translational profiling; expressed protein tag; EPT; kinase;

KW phosphatase; protease; protease inhibitor; transporter;

KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer;

KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;

KW leukaemia.

XX

OS Homo sapiens.

XX

ID ABU07250 standard; Protein; 288 AA.

XX AC ABU07250;

XX DT 29-JAN-2003 (First entry)

DE Human expressed protein tag (EPT) #1951.

XX KW Translational profiling; expressed protein tag; EPT; kinase;

KW phosphatase; protease; protease inhibitor; transporter;

KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer;

KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;

KW leukaemia.

XX

OS Homo sapiens.

XX

ID ABU07250 standard; Protein; 288 AA.

XX AC ABU07250;

XX DT 29-JAN-2003 (First entry)

DE Human expressed protein tag (EPT) #1951.

XX KW Translational profiling; expressed protein tag; EPT; kinase;

KW phosphatase; protease; protease inhibitor; transporter;

KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer;

KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;

KW leukaemia.

XX

OS Homo sapiens.

XX

ID ABU07250 standard; Protein; 288 AA.

XX AC ABU07250;

XX DT 29-JAN-2003 (First entry)

DE Human expressed protein tag (EPT) #1951.

XX KW Translational profiling; expressed protein tag; EPT; kinase;

KW phosphatase; protease; protease inhibitor; transporter;

KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer;

KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;

KW leukaemia.

XX

OS Homo sapiens.

XX

ID ABU07250 standard; Protein; 288 AA.

XX AC ABU07250;

XX DT 29-JAN-2003 (First entry)

DE Human expressed protein tag (EPT) #1951.

XX KW Translational profiling; expressed protein tag; EPT; kinase;

KW phosphatase; protease; protease inhibitor; transporter;

KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer;

KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;

KW leukaemia.

XX

OS Homo sapiens.

XX

ID ABU07250 standard; Protein; 288 AA.

XX AC ABU07250;

XX DT 29-JAN-2003 (First entry)

DE Human expressed protein tag (EPT) #1951.

XX KW Translational profiling; expressed protein tag; EPT; kinase;

KW phosphatase; protease; protease inhibitor; transporter;

KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer;

KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;

KW leukaemia.

XX

OS Homo sapiens.

XX

ID ABU07250 standard; Protein; 288 AA.

XX AC ABU07250;

XX DT 29-JAN-2003 (First entry)

DE Human expressed protein tag (EPT) #1951.

XX KW Translational profiling; expressed protein tag; EPT; kinase;

KW phosphatase; protease; protease inhibitor; transporter;

KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer;

KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;

KW leukaemia.

XX

OS Homo sapiens.

XX

ID ABU07250 standard; Protein; 288 AA.

XX AC ABU07250;

XX DT 29-JAN-2003 (First entry)

DE Human expressed protein tag (EPT) #1951.

XX KW Translational profiling; expressed protein tag; EPT; kinase;

KW phosphatase; protease; protease inhibitor; transporter;

KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer;

KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;

KW leukaemia.

XX

OS Homo sapiens.

XX

ID ABU07250 standard; Protein; 288 AA.

XX AC ABU07250;

XX DT 29-JAN-2003 (First entry)

DE Human expressed protein tag (EPT) #1951.

XX KW Translational profiling; expressed protein tag; EPT; kinase;

KW phosphatase; protease; protease inhibitor; transporter;

KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer;

KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;

KW leukaemia.

XX

OS Homo sapiens.

XX

ID ABU07250 standard; Protein; 288 AA.

XX AC ABU07250;

XX DT 29-JAN-2003 (First entry)

DE Human expressed protein tag (EPT) #1951.

XX KW Translational profiling; expressed protein tag; EPT; kinase;

KW phosphatase; protease; protease inhibitor; transporter;

KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer;

KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;

KW leukaemia.

XX

OS Homo sapiens.

XX

ID ABU07250 standard; Protein; 288 AA.

XX AC ABU07250;

XX DT 29-JAN-2003 (First entry)

DE Human expressed protein tag (EPT) #1951.

XX KW Translational profiling; expressed protein tag; EPT; kinase;

KW phosphatase; protease; protease inhibitor; transporter;

KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer;

KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;

KW leukaemia.

XX

OS Homo sapiens.

XX

ID ABU07250 standard; Protein; 288 AA.

XX AC ABU

XX 28-MAR-2002; 2002WO-US09671.  
 XX DE Human expressed protein tag (EPT) #1952.  
 XX PW Translational profiling; expressed protein tag; EPT; kinase;  
 XX KW phosphatase; protease; protease inhibitor; transporter;  
 PR 28-MAR-2001; 2001US-279495P; KW phosphatase; protease inhibitor; transporter;  
 PR 21-MAY-2001; 2001US-292544P; KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;  
 PR 08-AUG-2001; 2001US-310801P; KW major histocompatibility complex; myeloma; colon cancer;  
 PR 01-OCT-2001; 2001US-316370P; KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;  
 PR 04-DEC-2001; 2001US-336780P; KW leukaemia.  
 PR 20-FEB-2002; 2002US-358985P.  
 XX XX OS Homo sapiens.  
 PA XX PN WO200278524-A2.  
 XX PD 10-OCT-2002.  
 XX XX PR 28-MAR-2002; 2002WO-US09671.  
 XX XX PR 28-MAR-2001; 2001US-279495P.  
 PR 21-MAY-2001; 2001US-292544P.  
 PR 08-AUG-2001; 2001US-310801P.  
 PR 01-OCT-2001; 2001US-316370P.  
 PR 04-DEC-2001; 2001US-336780P.  
 PR 20-FEB-2002; 2002US-358985P.  
 PS PA (ZYCO-) ZYCOS INC.  
 XX PI Chicz RM, Tomlinson AJ, Urban RG;  
 XX DR WPI; 2003-040607/03.  
 XX PR New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.  
 XX PT PA (ZYCO-) ZYCOS INC.  
 XX PI Chicz RM, Tomlinson AJ, Urban RG;  
 XX DR WPI; 2003-040607/03.  
 XX PR New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.  
 XX PT PA (ZYCO-) ZYCOS INC.  
 XX PI Chicz RM, Tomlinson AJ, Urban RG;  
 XX DR WPI; 2003-040607/03.  
 XX PR New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing CC myeloma, colon cancer, gastric cancer, sarcoma, melanoma, CC lymphoma or leukaemia. These are also useful for screening agents for CC treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational CC profiling.  
 CC Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 288 AA;  
 CC Query Match 100.0%; Score 1149; DB 24; Length 288;  
 CC Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 CC Matches 216; Conservative 0; Mismatches 0; Gaps 0;  
 CC Indels 0; Gaps 0;  
 Qy 1 GLSHFCGVIVHVKVKEVATLSCGHNVSVEELAQTRIYQKEKKNVLTMSGDNNIWP 60  
 Db 27 GLSHFCGVIVHVKVKEVATLSCGHNVSVEELAQTRIYQKEKKNVLTMSGDNNIWP 86  
 Qy 61 YKNRTIIFDTNNLSIVIALRPSDEGTYECVVLKYKEKAFREHLAFTLISKADFPTPS 120  
 Db 87 YKNRTIIFDTNNLSIVIALRPSDEGTYECVVLKYKEKAFREHLAFTLISKADFPTPS 146  
 Qy 121 ISDPEIIPSNIRRIICSTSGGPEPHISWLENGEELNAINTVSQDPETELYAVSSKLDF 180  
 Db 147 ISDPEIIPSNIRRIICSTSGGPEPHISWLENGEELNAINTVSQDPETELYAVSSKLDF 206  
 Qy 181 NMNTNHSSMCLIKYGHLRVNOTFNNNTKQEHFPDN 216  
 Db 207 NMNTNHSSMCLIKYGHLRVNFNNNTKQEHFPDN 242  
 Qy 1 GLSHFCGVIVHVKVKEVATLSCGHNVSVEELAQTRIYQKEKKNVLTMSGDNNIWP 60  
 Db 27 GLSHFCGVIVHVKVKEVATLSCGHNVSVEELAQTRIYQKEKKNVLTMSGDNNIWP 86  
 Qy 61 YKNRTIIFDTNNLSIVIALRPSDEGTYECVVLKYKEKAFREHLAFTLISKADFPTPS 120  
 Db 87 YKNRTIIFDTNNLSIVIALRPSDEGTYECVVLKYKEKAFREHLAFTLISKADFPTPS 146  
 RESULT 23  
 ABU07251  
 ID ABU07251 standard; Protein: 288 AA.  
 XX AC ABU07251;  
 DT 29-JAN-2003 (first entry)  
 XX DT 121 ISDPEIIPSNIRRIICSTSGGPEPHISWLENGEELNAINTVSQDPETELYAVSSKLDF 180  
 DB 147 ISDPEIIPSNIRRIICSTSGGPEPHISWLENGEELNAINTVSQDPETELYAVSSKLDF 206

Oy	181	NMTTNHSPMCLIKYGLRVRNOTFNWNTTKQEHFPDN	216	Best Local Similarity 100.0%; Pred. No. 3.4e-103;
Db	207	NMTTNHSPMCLIKYGLRVRNOTFNWNTTKQEHFPDN	242	Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
<b>RESULT 24</b>				
ABU07254				Qy 1 GLSHFCSGVIVHTKEVATLSGHNSVEELAQTIVKQEVTLMSGDMMTIWPE 60
ID ABU07254	standard;	Protein:	288 AA.	Db 27 GLSHFCSGVIVHTKEVATLSGHNSVEELAQTIVKQEVTLMSGDMMTIWPE 86
XX				
AC ABU07254;				
XX				
DT 29-JAN-2003	(first entry)			
DE Human expressed protein tag (BPT) #1955.				
XX	Translational profiling; expressed protein tag; BPT; kinase;			
KW phosphatase; protease; protease inhibitor; transporter;				
KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;				
KW major histocompatibility complex; melanoma; colon cancer;				
KW gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;				
KW leukaemia.				
XX	Homo sapiens.			
OS				
PN WO200278524-A2.				
XX				
PD 10-OCT-2002.				
XX				
PF 28-MAR-2002; 2002WO-US09671.				
XX				
PR 28-MAR-2001; 2001US-279495P.				
PR 21-MAY-2001; 2001US-292544P.				
PR 08-AUG-2001; 2001US-310801P.				
PR 01-OCT-2001; 2001US-326370P.				
PR 04-DEC-2001; 2001US-336780P.				
PR 20-FEB-2002; 2002US-358985P.				
XX				
PA (ZYCO-) ZYCOS INC.				
XX				
PI Chicz RM, Tomlinson AJ, Urban RG;				
XX				
DR WPI; 2003-040607/03.				
XX				
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia -				
XX				
PS Example 2; SEQ ID No 1955; 134pp; English.				
XX				
CC The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor...				
CC The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (BPT) isolated from human tissue for translational profiling.				
CC Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at <a href="http://wipo.int/pub/published_pct_sequences">ftp.wipo.int/pub/published_pct_sequences</a> .				
XX Sequence 288 AA;				
SQ Query Match 100.0%; Score 1149; DB 24; Length 288;				



PR 28-MAR-2001; 2001US-279495P.  
 PR 2001US-292544P.  
 PR 08-AUG-2001; 2001US-310801P.  
 PR 01-OCT-2001; 2001US-326370P.  
 PR 04-DEC-2001; 2001US-336780P.  
 PR 20-FEB-2002; 2002US-358385P.  
 XX PA (ZYCO-) ZYCOS INC.  
 XX PI Chicz RM, Tomlinson AJ, Urban RG;  
 XX DR; 2003-040607/03.  
 XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia -  
 XX PS Example 2; SEQ ID No 1961; 134pp; English.  
 XX CC The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor.  
 CC The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. There are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling.  
 CC Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).  
 XX SQ Sequence 288 AA;  
 Query Match 100.0%; Score 1149; DB 24; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 216; Conservative 0; Mismatches 0; Gaps 0;  
 Indels 0;  
 Qy 1 GLSHFCGSVIVHTKEYKEVATLSCHNVVEELAQTRYWQKEKRMVLTMMSSDMNWIPE 60  
 Db 27 GLSHFCGSVIVHTKEYKEVATLSCHNVVEELAQTRYWQKEKRMVLTMMSSDMNWIPE 86  
 Note 61 YKNRIFIDITNNLSIVIALRPSDEGTYBCVVLKYKEKDAFKREHLAETVLSVKADEFPPS 120  
 Db 87 YKNRIFIDITNNLSIVIALRPSDEGTYBCVVLKYKEKDAFKREHLAETVLSVKADEFPPS 146  
 Qy 121 ISDFEIPTSNIRRICSTSGGFPPEHLSWLENGEELAINTVSDPTELYAVSSKDF 180  
 Db 147 ISDFEIPTSNIRRICSTSGGFPPEHLSWLENGEELAINTVSDPTELYAVSSKDF 206  
 Qy 181 NMTTNHSFMCILKIGHLRVNQTFWNTKQEHFPDN 216  
 Db 207 NMTTNHSFMCILKIGHLRVNQTFWNTKQEHFPDN 242  
 RESULT 28.  
 ID AB007261 standard; Protein; 288 AA.  
 XX AC AB007261;  
 XX DT 29-JAN-2003 (first entry)  
 XX Human expressed protein tag (EPT) #1962.  
 XX Translational profiling; expressed protein tag; EPT; kinase;  
 KW phosphatase; protease; protease inhibitor; transporter;  
 KW cytoskeletal protein; receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer;  
 KW gastric cancer; adenocarcinoma; sarcoma; lymphoma;  
 KW leukaemia.  
 XX OS Homo sapiens.  
 XX PN WO200278524-A2.  
 XX PD 10-OCT-2002.  
 XX PF 28-MAR-2002; 2002WO-US09671.  
 XX PR 28-MAR-2001; 2001US-279495P.  
 PR 21-MAY-2001; 2001US-392544P.  
 PR 08-AUG-2001; 2001US-310801P.  
 PR 01-OCT-2001; 2001US-326370P.  
 PR 04-DEC-2001; 2001US-336780P.  
 PR 20-FEB-2002; 2002US-358385P.  
 XX PA (ZYCO-) ZYCOS INC.  
 XX PI Chicz RM, Tomlinson AJ, Urban RG;  
 XX DR; 2003-040607/03.  
 XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia -  
 XX PS Example 2; SEQ ID No 1962; 134pp; English.  
 XX CC The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor.  
 CC The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling.  
 CC Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published\\_pct\\_sequences](ftp://wipo.int/pub/published_pct_sequences).  
 XX SQ Sequence 288 AA;  
 Query Match 100.0%; Score 1149; DB 24; Length 288;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 216; Conservative 0; Mismatches 0; Gaps 0;  
 Indels 0;  
 Qy 1 GLSHFCGSVIVHTKEYKEVATLSCHNVVEELAQTRYWQKEKRMVLTMMSSDMNWIPE 60  
 Db 27 GLSHFCGSVIVHTKEYKEVATLSCHNVVEELAQTRYWQKEKRMVLTMMSSDMNWIPE 86  
 Qy 61 YKNRIFIDITNNLSIVIALRPSDEGTYBCVVLKYKEKDAFKREHLAETVLSVKADEFPPS 120  
 Db 87 YKNRIFIDITNNLSIVIALRPSDEGTYBCVVLKYKEKDAFKREHLAETVLSVKADEFPPS 146  
 Qy 121 ISDFEIPTSNIRRICSTSGGFPPEHLSWLENGEELAINTVSDPTELYAVSSKDF 180  
 Db 147 ISDFEIPTSNIRRICSTSGGFPPEHLSWLENGEELAINTVSDPTELYAVSSKDF 206  
 Qy 181 NMTTNHSFMCILKIGHLRVNQTFWNTKQEHFPDN 216  
 Db 207 NMTTNHSFMCILKIGHLRVNQTFWNTKQEHFPDN 242  
 Qy 61 YKNRIFIDITNNLSIVIALRPSDEGTYBCVVLKYKEVATLSCHNVVEELAQTRYWQKEKRMVLTMMSSDMNWIPE 120  
 Db 87 YKNRIFIDITNNLSIVIALRPSDEGTYBCVVLKYKEVATLSCHNVVEELAQTRYWQKEKRMVLTMMSSDMNWIPE 86  
 Qy 121 ISDFEIPTSNIRRICSTSGGFPPEHLSWLENGEELAINTVSDPTELYAVSSKDF 180  
 Db 147 ISDFEIPTSNIRRICSTSGGFPPEHLSWLENGEELAINTVSDPTELYAVSSKDF 206  
 Qy 181 NMTTNHSFMCILKIGHLRVNQTFWNTKQEHFPDN 216  
 KW

Qy	1 GLSHFCSGYTHVTKVEKEYATLSCGHNVSEELAQTRIWKERKMKVLTMSGDNINWIPE 60
Db	27 GLSHFCSGYTHVTKVEKEYATLSCGHNVSEELAQTRIWKERKMKVLTMSGDNINWIPE 86
RESULT 29	
ABU07265	ABU07265 standard; Protein: 288 AA.
XX	XX
AC	AC
XX	XX
29-JAN-2003	(first entry)
Human expressed protein tag (EPT) #1966.	
XX	Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; leukaemia.
XX	
OS	Homo sapiens.
XX	
PN	WO200278524-A2.
PD	10-OCT-2002.
XX	
28-MAR-2002;	2002WO-US09671.
XX	
PR	2001US-279495P.
PR	2001US-292544P.
PR	2001US-310801P.
PR	2001US-326570P.
PR	2001US-336780P.
PR	2002US-358985P.
XX	
(ZYCO-)	ZYCOS INC.
XX	
PN	WO200278524-A2.
XX	
PD	10-OCT-2002.
XX	
28-MAR-2002;	2002WO-US09671.
XX	
PR	2001US-279495P.
PR	2001US-292544P.
PR	2001US-310801P.
PR	2001US-326570P.
PR	2001US-336780P.
PR	2002US-358985P.
XX	
Chicz RM, Tomlinson AJ, Urban RG;	
WPI; 2003-040607/03.	
XX	
PT	New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.
PT	
PT	The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling.
PS	Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at <a href="http://wipo.int/pub/published_pct_sequences">http://wipo.int/pub/published_pct_sequences</a> .
XX	
Sequence	288 AA;
Query Match	Score 1149; DB 24;
Best Local Similarity	Length 288;
Matches	Pred. No. 3.4e-103; Mismatches 0; Indels 0; Gaps 0;

lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling.

Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at: [ftp://wipo.int/pub/pct/pct\\_sequences](ftp://wipo.int/pub/pct/pct_sequences).

X X Example 2: SEQ ID No 1968; 134pp; English.  
X X The invention describes a purified polypeptide, which comprises a  
X X fragment of a kinase, phosphatase, protease, protease inhibitor,  
X X transporter, cytoskeletal protein, receptor or transcription factor.  
X X The invention is useful as an immunogen.

lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling.

Note: This sequence does not appear in the printed specification but was obtained in electronic form directly from WIPO at <ftp://wipo.int/pub/patent/pct/sequences>.

X Example 2: SEQ ID No 1968: 134pp; English.

X The invention describes a purified polypeptide, which comprises a  
X fragment of a kinase, phosphatase, protease, protease inhibitor,  
X transporter, cytoskeletal protein, receptor or transcription factor.  
X The polypeptide is useful as an immunogenic composition for eliciting  
X in a mammal an immunogenic response directed against any of the purified  
X polypeptide. The purified polypeptide, or the antibody that binds to  
X this polypeptide, is useful for treating cancer. The polypeptide is  
X also useful for identifying compounds that binds to a naturally  
X processed class I or class II MHC-binding polypeptide. The polypeptides  
X and poly nucleotides are particularly useful for treating or preventing  
X myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
X lymphoma or leukaemia. There are also useful for screening agents for  
X treating the above mentioned diseases. This sequence represents an  
X expressed protein tag (EPT) isolated from human tissue for translational  
X profiling.

X Note: This sequence does not appear in the printed specification but was  
X obtained in electronic format directly from WIPO at  
X <http://wipo.int/pub/published-pct-sequences>.

PR	01-OCT-2001; 2001US-326370P.	KW	gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma;
PR	04-DEC-2001; 2001US-336780P.	KW	leukaemia.
PR	20-FEB-2002; 2002US-35985P.	XX	
PA	(ZYCO-) ZYCOS INC.	OS	Homo sapiens.
XX		XX	
PI	Chicz RM, Tomlinson AJ, Urban RG;	PN	WO200278524-A2.
XX		XX	
DR	WPI; 2003-040607/03.	PD	10-OCT-2002.
XX		XX	
PR	New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia -	PR	28-MAR-2002; 2002WO-US09671.
PR		XX	28-MAR-2001; 2001US-279495P.
PR		PR	21-MAY-2001; 2001US-292544P.
PR		PR	08-AUG-2001; 2001US-310801P.
PR		PR	01-OCT-2001; 2001US-326370P.
XX		PR	04-DEC-2001; 2001US-336780P.
PS		PR	20-FEB-2002; 2002US-35985P.
XX		XX	
CC	Example 2: SEQ ID No 1969; 134pp; English.	PA	(ZYCO-) ZYCOS INC.
CC	The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor.	PI	Chicz RM, Tomlinson AJ, Urban RG;
CC	The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, sarcoma, melanoma, lymphoma or leukaemia. There are also useful for screening agents for expressed protein tag (EPT) isolated from human tissue for translational profiling.	XX	PAI 2003-040607/03.
CC	Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at <a href="http://ftp.wipo.int/pub/published_pct_sequences">ftp.wipo.int/pub/published_pct_sequences</a> .	XX	
XX		PS	Example 2: SEQ ID No 1970; 134pp; English.
CC	The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor.	XX	
CC	The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling.	XX	
CC	Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at <a href="http://ftp.wipo.int/pub/published_pct_sequences">ftp.wipo.int/pub/published_pct_sequences</a> .	XX	
SQ	Sequence 288 AA;	SQ	Sequence 288 AA;
	Query Match 100.0%; Score 1149; DB 24; Length 288;		Query Match 100.0%; Score 1149; DB 24; Length 288;
	Best Local Similarity 100.0%; Pred. No. 3. 4e-103; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Best Local Similarity 100.0%; Pred. No. 3. 4e-103; Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GLSHFCSGVIVHTKEVATLSCGHNYSVEELAQTRIYQKEKKMVTMMMSGDMNTWPE 60	Qy	1 GLSHFCSGVIVHTKEVATLSCGHNYSVEELAQTRIYQKEKKMVTMMMSGDMNTWPE 60
Db	27 GLSHFCSGVIVHTKEVATLSCGHNYSVEELAQTRIYQKEKKMVTMMMSGDMNTWPE 86	Db	27 GLSHFCSGVIVHTKEVATLSCGHNYSVEELAQTRIYQKEKKMVTMMMSGDMNTWPE 86
Qy	61 YKNRITIIFDTNNLSIVIALRPSDEGTYECVVLKYKEKDAFKREHLAETVLSYKADFTPS 120	Qy	61 YKNRITIIFDTNNLSIVIALRPSDEGTYECVVLKYKEKDAFKREHLAETVLSYKADFTPS 120
Db	87 YKNRITIIFDTNNLSIVIALRPSDEGTYECVVLKYKEKDAFKREHLAETVLSYKADFTPS 146	Db	87 YKNRITIIFDTNNLSIVIALRPSDEGTYECVVLKYKEKDAFKREHLAETVLSYKADFTPS 146
Qy	121 ISDFEIPSNIRIICSTSGGPDEPHLSWLENGBELNAINTVSQDPETELYAVSSKLDF 180	Qy	121 ISDFEIPSNIRIICSTSGGPDEPHLSWLENGBELNAINTVSQDPETELYAVSSKLDF 206
Db	147 ISDFEIPSNIRIICSTSGGPDEPHLSWLENGBELNAINTVSQDPETELYAVSSKLDF 216	Db	147 ISDFEIPSNIRIICSTSGGPDEPHLSWLENGBELNAINTVSQDPETELYAVSSKLDF 216
Qy	181 NMFTNHSFMCNLKIGHLRVNQFNWNTTKQEHFPDN 242	Qy	181 NMFTNHSFMCNLKIGHLRVNQFNWNTTKQEHFPDN 242
Db	207 NMFTNHSFMCNLKIGHLRVNQFNWNTTKQEHFPDN 242	Db	207 NMFTNHSFMCNLKIGHLRVNQFNWNTTKQEHFPDN 242
RESULT 33	AC ABU07229;	Qy	1 GLSHFCSGVIVHTKEVATLSCGHNYSVEELAQTRIYQKEKKMVTMMMSGDMNTWPE 60
ID ABU07269	XX	Db	27 GLSHFCSGVIVHTKEVATLSCGHNYSVEELAQTRIYQKEKKMVTMMMSGDMNTWPE 86
ID ABU07269 standard; Protein: 288 AA.	DT 29-JAN-2003 (first entry)	Qy	61 YKNRITIIFDTNNLSIVIALRPSDEGTYECVVLKYKEKDAFKREHLAETVLSYKADFTPS 120
DE Human expressed protein tag (EPT) #1970.	XX	Db	147 ISDFEIPSNIRIICSTSGGPDEPHLSWLENGBELNAINTVSQDPETELYAVSSKLDF 206
XX		Qy	181 NMFTNHSFMCNLKIGHLRVNQFNWNTTKQEHFPDN 242
KW	translational profiling; expressed protein tag; EPT; kinase;	Db	207 NMFTNHSFMCNLKIGHLRVNQFNWNTTKQEHFPDN 242
KW	phosphatase; protease; inhibitor; transporter;		
KW	cytoskeletal protein; receptor; transcription factor; cancer; MHC;		
KW	major histocompatibility complex; myeloma; colon cancer;		

RESULT 34  
 AAW41415 standard; Protein: 473 AA.  
 XX  
 AC AAW41415;  
 XX  
 DT 02-JUN-1998 (first entry)  
 XX Human B7.1-murine A5B7 F(ab')2 fusion protein.  
 XX Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;  
 XX cancer diagnosis; complementarity determining region.  
 XX  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Mus sp.  
 XX  
 PN WO974329-A1.  
 XX  
 PD 13-NOV-1997.  
 XX  
 PP 29-APR-1997; 97WO-GB01165.  
 XX  
 PR 14-FEB-1997; 97GB-0003103.  
 PR 04-MAY-1996; 96GB-0009405.  
 XX  
 PA (ZENECA LTD.  
 XX  
 PI Copley CG, Edge MD, Emery SC;  
 XX  
 DR WPI; 1997-558987/51.  
 DR N-PSDB; AAV1734/ .  
 XX  
 PT Anti-carcinoembryonic antigen antibody 806.077 Ab - used for  
 PT diagnosis and therapy of cancer.  
 XX  
 FS Reference Example 3; Page 190-193; 208pp; English.  
 XX  
 CC This sequence is the human B7.1-murine A5B7 F(ab')2 fusion protein  
 CC (AB7), and is an example of the antibody of the invention. The anti-body  
 CC is an anti-CEA (carcinoembryonic antigen) antibody (preferably  
 CC 806.077 Ab). Host cells or transgenic organisms transformed with DNA  
 CC encoding the antibody are used to make the antibody or conjugate. The  
 CC conjugate is used in a medicament suitable for intravenous  
 CC administration. The conjugate can be used for cancer therapy, selectively  
 CC killing tumour cells. The antibody can be used for in vivo or in vitro  
 CC diagnosis of cancer.  
 XX  
 SQ Sequence 473 AA;  
 Query Match 100.0%; Score 1149; DB 18; Length 473;  
 Best Local Similarity 100.0%; Pred. No. 6\_9e-103; Gaps 0;  
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GLSHFCGSVHVTKEVKEYATLSCGHNVSYEELAQTRIYQWERKRMVLTMMMSGDMNTWPE 60  
 Db 27 GLSHFCGSVHVTKEVKEYATLSCGHNVSYEELAQTRIYQWERKRMVLTMMMSGDMNTWPE 86  
 QY 61 YKNRTLFIDTNNLSIVILARPSDEGTYSCVVKYKEKDKREHLAETVLSKADFPPS 120  
 Db 87 YKNRTLFIDTNNLSIVILARPSDEGTYCCVVKYKEKDKREHLAETVLSKADFPPS 146  
 QY 121 ISDFPIPTSNIRRICSTSGGFPEPHSLNENGELNAINTVSQDPTELYAVSSKDF 180  
 Db 147 ISDFPIPTSNIRRICSTSGGFPEPHSLNENGELNAINTVSQDPTELYAVSSKDF 206  
 QY 181 NMTTNHSFMCLIKYGHRLRNYQTFWNTQEHFPDN 216  
 Db 207 NMTTNHSFMCLIKYGHRLRNYQTFWNTQEHFPDN 242